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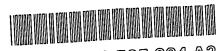
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(S) Imidazolinone resistant ahas mutants.

The present invention relates to monocot genes encoding a mutant AHAS enzyme that is specifically resistant to imidazolinone herbicides. Exemplary of these genes are corn DNA sequences which encode an amino acid substitution at position 621 of the wild-type AHAS enzyme. The mutant gene can be used to amino acid substitution at position 621 of the wild-type AHAS enzyme. The mutant gene can be used to transform other plants to herbicide resistance; in this regard, the invention also provides host cells and vectors containing the gene, which cells and vectors are useful in the transformation process.

This invention relates to novel DNA sequences that encode novel variant forms of acetohydroxy acid synthase enzyme (hereinafter AHAS). The AHAS enzyme is a critical enzyme routinely produced in a variety of plants and a broad range of microorganisms. Normal AHAS function is inhibited by imidazolinone herbicides; however, new AHAS enzymes encoded by the mutant DNA sequences function normally catalytically even in the presence of imidazolinone herbicides and, therefore, confer herbicide resistance upon the plant or microorganism containing them.

The novel DNA sequences are derived from corn and have a substitution of an amino acid at position 621 of the normal AHAS sequence. This substitution in the AHAS gene sequence results in a fully functional enzyme, but renders the enzyme specifically resistant to inhibition by a variety of imidazolinone herbicides. The availability of these variant sequences provides a tool for transformation of different crop plants to imidazolinone herbicide resistance, as well as providing novel selectable markers for use in other types of genetic transformation experiments.

BACKGROUND OF THE INVENTION

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The use of herbicides in agriculture is now widespread. Although there are a large number of available compounds which effectively destroy weeds, not all herbicides are capable of selectively targeting the undersirable plants over crop plants, as well as being non-toxic to animals. Often, it is necessary to settle for compounds which are simply less toxic to crop plants than to weeds. In order to overcome this problem, development of herbicide resistant crop plants has become a major focus of agricultural research.

An important aspect of development of herbicide-resistance is an understanding of the herbicide target, and then manipulating the affected biochemical pathway in the crop plant so that the inhibitory effect is avoided while the plant retains normal biological function. One of the first discoveries of the biochemical mechanism of herbicides related to a series of structurally unrelated herbicide compounds, the imidazolinones, the sulfonylureas and the triazolopyrimidines. It is now known (Shaner et al. Plant Physiol. 76: 545-546,1984; U.S. Patent No. 4,761,373) that each of these herbicides inhibits plant growth by interference with an essential enzyme required for plant growth, acetohydroxyacid synthase (AHAS; also referred to as acetolacetate synthase, or ALS). AHAS is required for the synthesis of the amino acids isoleucine, leucine and valine.

The AHAS enzyme is known to be present throughout higher plants, as well as being found in a variety of microorganisms, such as the yeast Saccharomyces cerevisiae, and the enteric bacteria, Escherichia coli and Salmonella typhimurium. The genetic basis for the production of normal AHAS in a number of these species has also been well characterized. For example, in both E. coli and S. typhimurium three isozymes of AHAS exist; two of these are sensitive to herbicides while a third is not. Each of these isozymes possesses one large and one small protein subunit; and map to the IIvIH, IIvGM and IIvBN operons. In yeast, the single AHAS isozyme has been mapped to the ILV2 locus. In each case, sensitive and resistant forms have been identified and sequences of the various alleles have been determined (Friden et. al., Nucl. Acid Res. 13: 3979-3993, 1985; Lawther et al., PNAS USA 78: 922-928, 1982; Squires et al., Nucl. Acids Res 811: 5299-5313, 1983; Wek et al; Nucl. Acids Res 13: 4011-4027, 1985; Falco and Dumas, Genetics 109, 21-35, 985; Falco et al, Nucl. Acids Res 13; 4011-4027, 1985).

In tobacco, AHAS function is encoded by two unlinked genes, SuRA and SuRB. There is substantial identity between the two genes, both at the nucleotide level and amino acid level in the mature protein, although the N-terminal, putative transit region differs more substantially (Lee et al, EMBO J. 7: 1241-1248, 1988). Arabidopsis, on the other hand, has a single AHAS gene, which has also been completely sequenced (Mazur et al., Plant Physiol. 85:1110-1117, 1987). Comparisons among sequences of the AHAS genes in higher plants indicates a high level of conservation of certain regions of the sequence; specifically, there are at least 10 regions of sequence conservation. It has previously been assumed that these conserved regions are critical to the function of the enzyme, and that retention of that function is dependent upon substantial sequence conservation.

It has been recently reported (U.S. Patent No. 5,013,659) that mutants exhibiting herbicide resistance possess mutations in at least one amino acid in one or more of these conserved regions. In particular, substitution of certain amino acids for the wild type amino acid at these specific sites in the AHAS protein sequence have been shown to be tolerated, and indeed result in herbicide resistance of the plant possessing this mutation, while retaining catalytic function. The mutations described therein encode either cross resistance for imidazolinones and sulfonylureas or sulfonylurea-specific resistance, but no imidazolinone-specific mutations were disclosed. These mutations have been shown to occur at both the SuRA and SuRB loci in tobacco; similar mutations have been isolated in Arabidopsis and yeast.

Imidazolinone-specific resistance has been reported elsewhere in a number of plants. U.S. Patent No.

4,761,373 generally described an altered AHAS as a basis of herbicide resistance in plants, and specifically disclosed certain imidazolinone resistant corn lines. Haughn et al. (Mol. Gen. Genet. 211:266-271, 1988) disclosed the occurrence of a similar phenotype in Arabidopsis. Sathasivan et al. (Nucl. Acid Res. 18:2188, 1990) identified the imidazolinone-specific resistance in Arabidopsis as being based on a mutation at position 653 in the normal AHAS sequence. In accordance with the present invention, a gene encoding imidazolinone-specific resistance in a monocot has now been isolated and determined to be associated with a single amino acid substitution in a wild-type monocot AHAS amino acid sequence.

SUMMARY OF THE INVENTION

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The present invention provides novel nucleic acid sequences encoding functional monocot AHAS enzymes insensitive to imidazolinone herbicides. The sequences in question comprise a mutation in the codon encoding the amino acid serine at position 621 in the corn (maize) AHAS sequence, or in the corresponding position in other monocot sequences. Other monocots, such as wheat, are also known to exhibit imidazolinone specific mutations (e.g., ATCC Nos. 40994-97). In corn, the wild type sequence has a serine at this position. In a preferred embodiment, the substitution is asparagine for serine, but alternate substitutions for serine include aspartic acid, glutamic acid, glutamine and tryptophane. Although the claimed sequences are originally derived from monocots, the novel sequences are useful in methods for producing imidazolinone resistant cells in any type of plant, said methods comprising transforming a target plant cell with one or more of the altered sequences provided herein. Alternatively, mutagenesis is utilized to create mutants in plant cells or seeds containing a nucleic acid sequence encoding an imidazolinone insensitive AHAS. In the case of mutant plant cells isolated in tissue culture, plants which possess the imidazolinone resistant or insensitive trait are then regenerated. The invention thus also encompasses plant cells, bacterial cells, fungal cells, plant tissue cultures, adult plants, and plant seeds that possess a mutant nucleic acid sequence and which express functional imidazolinone resistant AHAS enzymes.

The availability of these novel herbicide resistant plants enables new methods of growing crop plants in the presence of imidazolinones. Instead of growing non-resistant plants, fields may be planted with the resistant plants produced by mutation or by transformation with the mutant sequences of the present invention, and the field routinely treated with imidazolinones, with no resulting damage to crop plants.

The mutant nucleic acids of the present invention also provide novel selectable markers for use in transformation experiments. The nucleic acid sequence encoding a resistant AHAS is linked to a second gene prior to transfer to a host cell, and the entire construct transformed into the host. Putative transformed cells are then grown in culture in the presence of inhibitory amounts of herbicide; surviving cells will have a high probability of having successfully acquired the second gene of interest. Alternately, the resistant AHAS gene can be cotransformed on an independent plasmid with the gene of interest, whereby about 50% of all transformants can be expected to have received both genes.

The following definitions should be understood to apply throughout the specification and claims. A "functional" or "normal" AHAS enzyme is one which is capable of catalyzing the first step in the pathway for synthesis of the essential amino acids isoleucine, leucine and valine. A "wild-type" AHAS sequence is a sequence present in an imidazolinone sensitive member of a given species. A "resistant" plant is one which produces a mutant but functional AHAS enzyme, and which is capable of reaching maturity when grown in the presence of normally inhibitory levels of imidazolinone. The term "resistant", as used herein, is also intended to encompass "tolerant" plants, i.e., those plants which phenotypically evidence adverse, but not lethal, reactions to the imidazolinone.

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BRIEF DESCRIPTION OF THE FIGURES

Figure 1: AHAS enzyme activity in 10-day old maize seedlings (corn lines A619 or XI12) in the presence of imazethapyr (Pursuit™ A) or chlorsulfuron (Oust™ B). Herbicide resistant AHAS activity is calculated as percentage of AHAS activity in the absence of inhibitor. The standard error between experimets is 10%.

Figure 2: Southern analysis of genomic clones in phage EMBL3. Phages 12-1A (from W22), 12-7A, 18-8A, 12-11, and 12-17A (From XI12) are digested with Xbal or Sall, separated on a 1% agarose gel, transfered onto nitrocellulose and hybridized with an AHAS cDNA fragment as probe.

Figure 3: Southern analysis of genomic DNA from corn lines XI12, XA17, QJ22, A188 and B73. The DNA is digested with Xbal, separated on a 1% agarose gel, transferred onto nitrocellulose and hybridized with an AHAS cDNA fragment as probe.

Figure 4: Restriction map of plasmid pCD8A. The mutant AHAS gene from XI12 was subcloned as a

8kb Pstl fragment into vector pKS(+). The location and orientation of the AHAS gene is indicated by an arrow. The restriction sites of Pstl, Xhol, HindIII, Xbal and Clal are represented by symbols.

Figure 5: Nucleotide sequencing gel of the non-coding strand (A) and the double stranded DNA sequence (B) of AHAS clones W22/4-4, B73/10-4 and XI12/8A in the region of amino acids 614 to 633. The position of the cytosine to thymidine transition is indicated by an arrow.

Figure 6: Nucleotide and deduced amino acid sequences of the XI12/8A mutant AHAS gene.

Figure 7: Nucleotide sequence alignment of XI12/8A, B73/7-4 and W22/1A als2 genes. (*) marks the base change causing the mutation at position 621, (#) differences from the B73/7-4 sequence and (>) represents silent changes.

Figure 8: Amino acid sequences and alignment of XI12/BA, B73/7-4 and W22/1A als2 genes. (*) marks the mutation at position 621, (#) marks differences from the B73/7-4 sequence, and (>) represents silent changes.

DETAILED DESCRIPTION OF THE INVENTION

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The gene of the present invention is isolatable from corn maize line XI12 (seed deposited with the American Type Culture Collection as Accession Number 75051), and has been inserted into plasmid pXI12/8A (deposited with the American Type Culture Collection as Accession Number 68643). It is also isolatable from any other imidazolinone-specific herbicide resistant mutant, such as the corn line QJ22 (deposited as a cell culture with the American Type Culture Collection as Accession Number 40129), or the various wheat plants (seed deposited with the American Type Collection as Accession Numbers 40994, 40995, 40996, or 40997). A genomic DNA library is created, for example, in phage ENBL-3 with DNA from one of the imidazolinone resistant mutants, preferably one which is homozygous for the resistance trait, and is screened with a nucleic acid probe comprising all or a part of a wild-type AHAS sequence.

In maize, the AHAS gene is found at two loci, als1 and als2 (Burr and Burr, Trends in Genetics 7:55-61, 1991); the homology between the two loci is 95% at the nucleotide level. The mutation in XI12 is mapped to locus als2 on chromosome 5, whereas the nonmutant gene is mapped to locus als1 on chromosome 4 (Newhouse et al., "Imidazolinone-resistant crops". In The Imidazolinone Herbicides, Shaner and O'Connor (Eds.), CRC Press, Boca Raton, FL, in Press) Southern analysis identifies some clones containing the mutant als2 gene, and some containing the non-mutant als1 gene. Both types are subcloned into sequencing vectors, and sequenced by the dideoxy sequencing method.

Sequencing and comparison of wild type and mutant AHAS genes shows a difference of a single nucleotide in the codon encoding the amino acid at position 621 (Figure 5). Specifically, the codon AGT encoding serine in the wild type is changed to AAT encoding asparagine in the mutant AHAS (Figure 8). The mutant AHAS gene is otherwise similar to the wild type gene, encoding a protein having 638 amino acids, the first 40 of which constitute a transit peptide which is thought to be cleaved during transport into the chloroplast in vivo. The sequence of the als1 non-mutant gene from XI12 appears to be identical to the als1 gene from B73.

The mutant genes of the present invention confer resistance to imidazolinone herbicides, but not to sulfonylurea herbicides. Types of herbicides to which resistance is conferred are described for example in U.S. Patent Nos. 4,188,487; 4,201,565; 4,221,586; 4,297,128; 4,554,013; 4,608,079; 4,638,068; 4,747,301; 4,650,514; 4,698,092; 4,701,208; 4,709,036; 4,752,323; 4,772,311; and 4,798,619.

It will be understood by those skilled in the art that the nucleic acid sequence depicted in Figure 6 is not the only sequence which can be used to confer imidazolinone-specific resistance. Also contemplated are those nucleic acid sequences which encode an identical protein but which, because of the degeneracy of the genetic code, possess a different nucleotide sequence. The invention also encompasses genes encoding AHAS sequences in which the aforestated mutation is present, but which also encode one or more silent amino acid changes in portions of the molecule not involved with resistance or catalytic function. Also contemplated are gene sequences from other imidazolinone resistant monocots which have a mutation in the corresponding region of the sequences.

For example, alterations in the gene sequence which result in the production of a chemically equivalent amino acid at a given site are contemplated; thus, a codon for the amino acid alanine, a hydrophobic amino acid, can readily be substituted by a codon encoding another hydrophobic residue, such as glycine, or may be substituted with a more hydrophobic residue such as valine, leucine, or isoleucine. Similarly, changes which result in substitution of one negatively charged residue for another, such as aspartic acid for glutamic acid, or one positively charged residue for another, such as lysine for arginine, can also be expected to produce a biologically equivalent product. The invention also encompasses chimaeric genes, in which the substituted portion of the corn AHAS gene is recombined with unaltered portions of the normal AHAS genes

from other species. Thus, throughout the specification and claims, wherever the term "imidazolinone-specific resistant corn AHAS gene" is used, it is intended to cover each of these alternate embodiments as well as the sequence of Figure 6.

Isolated AHAS DNA sequences of the present invention are useful to transform target crop plants, and thereby confer imidazolinone resistance. A broad range of techniques currently exist for achieving direct or indirect transformation of higher plants with exogenous DNA, and any method by which the novel sequence can be incorporated into the host genome, and stably inherited by its progeny, is contemplated by the present invention. The imidazolinone specific resistance trait is inherited as a single dominant nuclear gene. The level of imidazolinone resistance is increased when the gene is present in a homozygous state; such corn plants, for example, have a resistance level of about 1,000 times that of a non-resistant plant. Plants heterozygous for the trait, however, have a resistance of about 50-500 times that of a non-resistant plant.

Transformation of plant cells can be mediated by the use of vectors. A common method of achieving transformation is the use of Agrobacterium tumefaciens to introduce a foreign gene into the target plant cell. For example, the mutant AHAS sequence is inserted into a plasmid vector containing the flanking sequences in the Ti-plasmid T-DNA. The plasmid is then transformed into E. coli. A triparental mating among this strain, an Agrobacterium strain containing a disarmed Ti-plasmid containing the virulence functions needed to effect transfer of the AHAS containing T-DNA sequences into the target plant chromosome, and a second E. coli strain containing a plasmid having sequences necessary to mobilize transfer of the AHAS construct from E. coli to Agrobacterium is carried out. A recombinant Agrobacterium strain, containing the necessary sequences for plant transformation is used to infect leaf discs. Discs are grown on selection media and successfully transformed regenerants are identified. The recovered plants are resistant to the effects of herbicide when grown in its presence. Plant viruses also provide a possible means for transfer of exogenous DNA.

Direct uptake of plant cells can also be employed. Typically, protoplasts of the target plant are placed in culture in the presence of the DNA to be transferred, and an agent which promotes the uptake of DNA by protoplast. Useful agents in this regard are polyethylene glycol or calcium phosphate.

Alternatively, DNA uptake can be stimulated by electroporation. In this method, an electrical pulse is used to open temporary pores in a protoplast cell membrane, and DNA in the surrounding solution is then drawn into the cell through the pores. Similarly, microinjection can be employed to deliver the DNA directly into a cell, and preferably directly into the nucleus of the cell.

In each of the foregoing techniques, transformation occurs in a plant cell in culture. Subsequent to the transformation event, plant cells must be regenerated to whole plants. Techniques for the regeneration of mature plants from callus or protoplast culture are now well known for a large number of different species (see, e.g., Handbook of Plant Cell Culture, Vols. 1-5, 1983-1989 McMillan, N.Y.) Thus, once transformation has been achieved, it is within the knowledge in the art to regenerate mature plants from the transformed plant cells.

Alternate methods are also now available which do not necessarily require the use of isolated cells, and therefore, plant regeneration techniques, to achieve transformation. These are generally referred to as "ballistic" or "particle acceleration" methods, in which DNA coated metal particles are propelled into plant cells by either a gunpowder charge (Klein et al., Nature 327: 70-73, 1987) or electrical discharge (EPO 270 356). In this manner, plant cells in culture or plant reproductive organs or cells, e.g. pollen, can be stably transformed with the DNA sequence of interest.

In certain dicots and monocots direct uptake of DNA is the preferred method of transformation. For example, in corn, the cell wall of cultured cells is digested in a buffer with one or more cell wall degrading enzymes, such as cellulase, hemicellulase and pectinase, to isolate viable protoplasts. The protoplasts are washed several times to remove the enzymes, and mixed with a plasmid vector containing the gene of interest. The cells can be transformed with either PEG (e.g. 20% PEG 4000) or by electroporation. The protoplasts are placed on a nitrocellulose filter and cultured on a medium with embedded corn cells functioning as feeder cultures. After 2-4 weeks, the cultures in the nitrocellulose filter are placed on a medium containing about $0.32~\mu\text{M}$ of the imidazolinone and maintained in the medium for 1-2 months. The nitrocellulose filters with the plant cells are transferred to fresh medium with herbicides and nurse cells every two weeks. The untransformed cells cease growing and die after a few weeks.

The present invention can be applied to transformation of virtually any type of plant, both monocot and dicot. Among the crop plants for which transformation to herbicide resistance is contemplated are corn, wheat, rice, millet, oat, barley, sorghum, sunflower, sweet potato, alfalfa, sugar beet, Brassica species, tomato, pepper, soybean, tobacco, melon, squash, potato, peanut, pea, cotton, or cacao. The novel sequences may also be used to transform ornamental species, such as rose, and woody species, such as pine and poplar.

The novel sequences of the invention also are useful as selectable markers in plant genetics studies. For example, in plant transformation, sequences encoding imidazolinone resistance could be linked to a gene of interest which is to be used to transform a target imidazolinone sensitive plant cell. The construct comprising both the gene of interest and the imidazolinone resistant sequence are introduced into the plant cell, and the plant cells are then grown in the presence of an inhibitory amount of an imidazolinone. Alternately, the second gene of interest can be cotransformed, on a separate plasmid, into the host cells. Plant cells surviving such treatment presumably have acquired the resistance gene as well as the gene of interest, and therefore, only transformants survive the selection process with the herbicide. Confirmation of successful transformation and expression of both genes can be achieved by Southern hybridization of genomic DNA, by PCR or by observation of the phenotypic expression of the genes.

The invention is further illustrated by the following non-limiting examples.

EXAMPLES

1. Confirmation of Whole Plant Herbicide Resistance in XI12

XI12 plants are treated with herbicides at 10 days to the V3 leaf stage (4-5 leaves, of which 3 have visible ligules). Imazethapyr is applied at rates of 2000, 500, 250, 125 and 62.5 g/ha. Chlorsulfuron is applied at 32, 16, 8, 4 and 2 g/ha. Plants are treated postemergence at a spray volume of 400 l/ha. After spraying, plants are placed in the greenhouse for further observation.

XI12 plants are unaffected at all rates of imazethapyr treatment; however, no visible increased resistance to chlorsulfuron is noted. Thus, XI12 displays selective resistance to the imidazolinone at the whole plant level (See Figure 1).

The resistance in XI12 is also shown to be inherited as a single dominant allele of a nuclear gene. Heterozygous resistant XI12 are selfed, and the selfed progeny segregate in the 3 resistant:1 susceptible ratio expected for a single dominant allele of a nuclear gene. In this study, the segregating seedlings are sprayed postemergence with lethal doses of imazethapyr (125 or 250 g/ha) following spraying protocols described above, to establish segregation for resistance.

o 2. AHAS Extraction

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Seeds of XI12 are sown in soil in a greenhouse maintained at day/night temperature of 80°C and 15 hour photoperiod. Plants are harvested two weeks after planting. The basal portion of the shoot is used for the extraction of AHAS. 5 g of the tissue is powdered in liquid nitrogen and then homogenized in AHAS assay buffer comprising 100 mM potassium phosphate buffer (pH 7.5) containing 10 mM pyruvate, 5 mM MgCl₂, 5 mM EDTA, 100 uM FAD (flavin adenine dinucleotide), 1 mM valine, 1 mM leucine, 10% glycerol and 10 mM cysteine. The homogenate is centrifuged at 10,000 rpm for 10 minutes and 3 ml of the supernatant are applied onto an equilibrated Bio-Rad Econo-Desalting column (10 DG) and eluted with 4 ml AHAS assay buffer.

AHAS activity is measured by estimation of the product, acetolactate, after conversion by decarbox-ylation in the presence of acid to acetoin. Standard reaction mixtures contain the enzyme in 50 mM potassium phosphate (pH 7.0) containing 100 mM sodium pyruvate, 10 mM MgCl₂, 1 mM thiamine pyrophosphate, 10 uM FAD, and appropriate concentrations of different inhibitors. This mixture is incubated at 37°C for 1 to 3 hours depending upon the experiment. At the end of this incubation period, the reaction is stopped with the addition of H₂SO₄ to make a final concentration of 0.85% H₂SO₄ in the tube. The reaction product is allowed to decarboxylate at 60°C for 15 minutes. The acetoin formed is determined by incubating with creatine (0.17%) and 1-naphthol (1.7% in 4N NaOH). The absorption of color complex formed is measured at 520 nm.

AHAS activity from B73, A619, or other wild-type maize lines is highly sensitive to inhibition by imazethapyr (PURSUIT™) with an I₅₀ of 1 uM (See Figure 1). Contrary to this observation, XI12 shows 70-80% of enzyme activity at the highest concentrations (100 µM) of PURSUIT™ or ARSENAL™ (imazepyr), and about 70% in the presence of SCEPTER™ (imazequin). This result shows a 100-fold increase in tolerance of AHAS activity from XI12 to imazethapyr as compared to the in vitro AHAS activity from A619. sensitivity of AHAS activity from the two lines to sulfonylureas gives a different picture. In the presence of OUST™ (sulfometuron methyl), at 100 nM, AHAS activity of XI12 is only 15-20%. AHAS activity of A619 in the presence of OUST™ IS 5-10%, and in the presence of PURSUIT™ is 15-20% (See Figure 1).

3. Cloning of XI12 AHAS Genes

Seeds of the XI12 mutant derived from an imidazolinone resistant corn tissue culture line are planted; plants obtained therefrom appear to be segregating for the mutant AHAS phenotype. In order to obtain homozygous resistant seed material, a population of XI12 mutant plants are selfed. After selecting for herbicide resistance for three consecutive growing seasons, the seeds are homozygous for the mutant AHAS gene. Homozygous seeds are collected and used to grow seedlings to be used in AHAS gene isolation.

DNA is extracted from 7 days old etiolated seedlings of a homozygous XI12 line. 60 g of plant tissue is powdered in liquid nitrogen, and transfered into 108 ml DNA extraction buffer (1.4 M NaCl, 2.0% Ctab (hexadecyl trimethyl ammonium bromide), 100 mM tris-Cl pH 8.0, 20 mM EDTA, 2% Mercaptoethanol) and 54 ml water. After incubation at 50-60°C for 30 minutes the suspension is extracted with an equal amount of chloroform. The DNA is precipitated by adding an equal amount of precipitation buffer (1% Ctab, 50 mM Tris-Cl pH 8.0, 10 mM EDTA). To purify the genomic DNA, a high speed centrifugation in 6.6M CsCl and ethidium bromide is performed (Ti80 rotor, 50,000 rpm, 20°C, 24 hours). The purified DNA is extracted with salt saturated Butanol and dialyzed for 25 hours against 3 changes of 1 I dialysis buffer (10 mM Tris-Cl Ph 8.0, 1 mM EDTA, 0.1M NaCl). The concentration of the XI12 genomic DNA is determined spectrophotometrically to be 310 mg/ml. The yield is 0.93 mg.

The XI12 genomic DNA is used to create a genomic library in the phage EMBL-3. The DNA is partially digested with Mbol and the fragments are separated on a sucrose gradient to produce size range between 8 to 22 kb before cloning into the BamHl site of EMBL-3. After obtaining 2.1 x 10⁶ independent clones, the library is amplified once. The titer of the library is determined 9 x 10¹⁰ pfu/ml.

To obtain probes for analysis of the XI12 library, a W22 (wild-type) cDNA library in lambda gt11, purchased from Clontech Inc., CA, is screened with an 800 nt BamH1 probe isolated from Arabidopsis AHAS genomic clone. The phages are plated in a density of 50,000 pfu/15 cm plate, transferred onto nitrocellulose filters, prehybridized in 6x SSC, 0.2% SDS for 2 hours and hybridized with the Arabidopsis AHAS probe in 6x SSC, 0.2% SDS overnight. One positive phage is identified, further purified and used for subcloning of a 1.1 kb EcoRI fragment. The 1.1 kb EcoRI fragment is subcloned into pGemA-4 and used as a probe to identify the XI12 AHAS genes.

The XI12 genomic library is plated on 12 15-cm plates (concentration of 50,000 pfu/plate) and is screened with the W22 AHAS cDNA probe. The filters are prehybridized (2 hours) and hybridized (over night) in Church buffer (0.5 M Na Phosphate, 1 mM EDTA, 1% BSA, 7% SDS) at 65°C and washed at 65°C in 2x SSC, 0.2% SDS and 0.3 x SSC, 0.2% SDS. 12 positive plaques are obtained from a total of 7.5 x 10⁵ pfu screened and 5 positive clones are further purified and isolated according to Chisholm (BioTechniques 7:21-23, 1989). Southern analysis (See Figure 2) showed that the phage clones represented two types of ĀHAS clones: Type-1 clones contain one large Xbal (>6.5 kb) fragment hybridizing to the AHAS cDNA probe, Type-2 clones contained two 2.7 and 3.7 kb Xbal fragments hybridizing to the AHAS cDNA probe. Genomic Southern of XI12 DNA demonstrated, that the Xbal fragments obtained by digesting genomic DNA and by hybridizing to the AHAS cDNA probe correspond to the Xbal fragments identified in the XI12 phage clones (See Figure 3). Restriction digest and Southern Analysis also demonstrate that of the 5 AHAS clones, one clone represents the mutant als2 genes and four represent the als1 gene.

The AHAS genes corresponding to the mutant locus located on chromosome 5 (clone 12/8A) and the non-mutant locus located on chromosome 4 (clone 12/17A) are subcloned as a Pstl fragment (clone 12/8A) or as Xbal fragment (12/17A) into the sequencing vector pBluescript II KSm13(+) (pKS+; Stratagene). Both 2.7 kb and 3.7 kb Xbal fragments from phage 12/17A contain one complete copy of AHAS genes which are identified. The sequence of each is obtained by dideoxy sequencing (Pharmacia T7 sequencing Kits) using primers complementary to the AHAS coding sequence.

The methods of DNA extraction, cloning of the genomic library and screening of the library are as described for the XI12 genomic DNA. The B73 AHAS genes are subcloned into the sequencing vector pKS+ as Xbal fragments and are sequenced. The sequence is obtained by dideoxy sequencing, using primers complementary to the AHAS coding sequence as described for the SI12 AHAS genes.

A W22 genomic library in EMBL3 purchased from Clontech Inc., CA is screened. The phages are plated in a density of 50,000 pfu/7 inch plate, transferred onto nitrocellulose filters, and hybridized with the W22 AHAS cDNA probe described above (prehybridization and hybridization conditions: 6 x SSC, 0.5% SDS, 1X Denhard's 100 mg/ml calf thymus DNA, 65°C, washing conditions: 3X x SSC, 0.2% SDS for 2 hours at 65°C, and 0.3 x SSC, 0.2% SDS for 2 hours). Two positive phages (12/1A and 12/4-4) are identified and further purified.

The W22 genomic clone 12/1A is subcloned as two 0.78 kb (pGemA-4) and 3.0 kb (pGemA-14; Promega) Sall fragments into the vector pGem-A2, and as a 6.5 kb Xbal fragment into the vector pKS+ (pCD200). The coding strand sequence of the W22 AHAS gene is obtained by dideoxy sequencing of

nested deletions created from subclones pGem A-14 and pGem A-4 of phage 12-1A. This sequence is used to design oligonucleotides complementary to the AHAS non-coding strand. The sequence of the non-coding strand is obtained by dideoxy sequencing of clone pCD200 using primers complementary to the coding strand. Upon complementing the sequencing of the W22 AHAS gene, primers of both DNA strands are designed and used for the sequencing of the AHAS genes isolated from the XI12 and B73 genomic libraries.

4. Cloning of QJ22 AHAS Genes

The sequence of the gene encoding AHAS in the maize line QJ22, which is selectively resistant to imidazolinones, is also determined. A genomic library of QJ22 is prepared in an EMBL3 vector. A library of 800,000 phage is screened with an 850 nucleotide Sall/Clal fragment isolated from an AHAS clone (A-4) derived from the wild-type maize line W22. Five positive phages are picked and submitted to a second round of screening to partially purify the phage. The partially purified phage are analyzed by PCR to determine if any clones represent the QJ22 alsl gene. Such clones are identified as a 3.7kb Xbal fragment with a gene specific Smal site at position $\overline{49}5$. The second screen indicates the presence of a single positive clone with these characteristics.

The PCR product is purified using a commercial kit (Magic PCR Preps) from Promega, and the purified DNA is sequenced with a Taq polymerase sequencing system "fmol", also from Promega Sequence analysis of both strands of the DNA of the QJ22 mutant AHAS shows a nucleotide transition from G to A in the codon for amino acid 621. This mutation is identical to the one seen in XI12 and the remainder of the sequence is typical of an als1 gene.

RESULTS

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The sequence of the mutant AHAS genes is compared with the sequences obtained from the wild type corn lines B73 and W22 (See Figure 7). The XI12 mutant gene (XI12/8A) and the QJ22 mutant gene and the wild type gene are identical except for the amino acid change at position 621, causing a single nucleotide transition from AGT to AAT (See Figure 8). The XI12 mutant XI12/8A and the wild-type B73/7-4 gene show an additional difference at position 63. On the other hand, the non-mutant XI12 AHAS gene cloned in XI12/17A is completely homologous to the corresponding B73/10-2 in the region coding for the mature AHAS protein (data not shown).

DEPOSIT OF BIOLOGICAL MATERIALS

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The following biological materials were deposited with the American Type Culture Collection, 12301 Parklawn Drive, Rockville, Maryland, 20857, as follows:

E. coli XLI Blue harboring plasmid pX12/8A, deposited on July 3, 1991, Accession Number ATCC 68643

XI12 corn seed deposited on July 16, 1991, Accession Number ATCC 75051.

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Sequence Listings

5	Seg	uenc	e ID	No.	: 1								
	Seq	uenc	в туј	e:	Nuc:	leot:	ide :	and 2	Amin	o Ac	id		
10	Seg	uenc	e Lei	ngth:	: 1	969 I	BP's	and	638	Ami	no A	cids	
15	Str	ande	dnes	3: £	sing:	l e							
	Topo	olog	y : 1	Linea	9. T								٠
20	ori	gina	l So	ırce	Orga	anisı	n: <u>1</u>	<u>Zea</u> 1	<u>nays</u>				
25	Prop	pert:	ies:	Hei	rbic:	ide 1	Resi	stani	t ah	AS E	n z ym	2	
20	AAC	CCTC	GCG (ceec	CTCC	ga Gi	ACAG	CCGC	C GC	AACC			36
30	ATG	GCC	ACC	GCC	GCC	GCC	GCG	TCT	ACC	GCG	CTC	ACT	72
	Met	Ala	Thr	Ala	Ala	Ala	Ala	Ser	Thr	Ala	Leu	Thr	
	1				5					10			
35													
												CGG	108
	GIĀ	Ala		Thr	WIS	WI8	Pro	_	WIÐ	Arg	Arg	arg	
40			15					20					
	GCG	CAC	CTC	CTG	GCC	ACC	CGC	CGC	GCC	CTC	GCC	GCG	144
				Leu								Ala	
45	25					30	-	_			35		
	CCC	ATC	AGG	TGC	TCA	GCG	GCG	TCA	CCC	GCC	ATG	CCG	180
50	Pro	Ile	Arg	Cys	Ser	Ala	Ala	ser		Ala	Met	Pro	
				40					45				

5	ATG	GCT	ccc	CCG	GCC	ACC	CCG	CTC	CGG	CCG	TGG	GGC	216	
	Met	Ala	Pro	Pro	Ala	Thr	Pro	Leu	Arg	Pro	Trp	Gly		
		50					55					60		
10	ccc	ACC	GAT	ccc	CGC	AAG	GGC	GCC	GAC	ATC	CTC	GTC	252	
	Pro	Thr	Asp	Pro	Arg	Lys	Gly	Ala	Asp	Ile	Leu	Val		
					65					70				
15														
	GAG	TCC	CTC	GAG	CGC	TGC	GGC	GTC	CGC	GAC	GTC	TTC	288	
	Glu	Ser	Leu	Glu	Arg	Cys	Gly	Val	Arg	Asp	Val	Phe		
20			75					80						
20														
	GCC	TAC	ccc	GGC	GGC	GCG	TCC	ATG	GAG	ATC	CAC	CAG	324	
	Ala	Tyr	Pro	Gly	Gly	Ala	Ser	Met	Glu	Ile	His	Gln		
25	85					90					95			
	GCA	CTC	ACC	CGC	TCC	ccc	GTC	ATC	GCC	AAC	CAC	CTC	360	
30	Ala	Leu	Thr	Arg	Ser	Pro	Val	Ile	Ala	Asn	His	Leu		
				100					105					
35	TTC	CGC	CAC	GAG	CAA	GGG	GAG	GCC	TTT	GCG	GCC	TCC	396	
00	Phe	Arg	His	Glu	Gln	Gly	Glu	Ala	Phe	Ala	Ala	8er		
		110					115					120		
40	GGC	TAC	GCG	CGC	TCC	TCG	GGC	CGC	GTC	GGC	GTC	TGC	432	
	Gly	Tyr	Ala	Arg	ser	Ser	Gly	Arg	Val	Gly	Val	Cys		
					125					130				
45														
	ATC	GCC	ACC	TCC	GGC	CCC	GGC	GCC	ACC	AAC	CTT	GTC	468	
	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val		
50			135					140						
	TCC	GCG	CTC	GCC	GAC	GCG	CTG	CTC	GAT	TCC	GTC	CCC	504	
	Ser	Ala	Leu	Ala	Asp	Ala	Leu	Leu	Asp	Ser	Val	Pro		
55	145					150					155			

5	ATG	GTC	GCC	ATC	ACG	GGA	CAG	GTG	CCG	CGA	CGC	ATG	540
·	Met	Val	Ala	Ile	Thr	Gly	Gln	٧al	Pro	Arg	Arg	Met	
				160					165				
10	ATT	GGC	ACC	GAC	GCC	TTC	CAG	GAG	ACG	ccc	ATC	GTC	576
	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Thr	Pro	Ile	AST	
		170					175					180	
15													•
	GAG	GTC	ACC	CGC	TCC	ATC	ACC	AAG	CAC	AAC	TAC	CTG	612
	Glu	Val	Thr	Arg	ser	Ile	Thr	Lys	His	Asn	Tyr	Leu	
20					185					190			
	GTC	CTC	GAC	GTC	GAC	GAC	ATC	ccc	CGC	GTC	GTG	CAG	648
	Val	Leu	Asp	Val	Asp	Asp	Ile	Pro	Arg	A9J	val	Gln	
25			195					200					
	GAG	GCT	TTC	TTC	CTC	GCC	TCC	TCT	GGT	CGA	CCG	GGG	684
30	Glu	Ala	Phe	Phe	Leu	Ala	Ser	Ser	Gly	Arg	Pro	Gly	
	205					210					215		
35	CCG	GTG	CTT	GTC	GAC	ATC	CCC	AAG	GAC	ATC	CAG	CAG	720
	Pro	Val	Leu		Asp	Ile	Pro	Lys	Asp	Ile	Gln	Gln	
				220					225				
40													
40									AAG -				756
	Gln		Ala	Val	Pro	Val	_	Asp	Lys	Pro	net		
		230					235					240	
45													500
												CCT	792
	Leu	Pro	Gly	TYX		Ala	Arg	Leu	Pro		Pro	bro.	
50					245					250			
												48B	000
									CTG				828
55	Ala	Thr		Leu	Leu	Glu	Gln		Leu	arg	Leu	AST	
33			255					260					

	GGT	GAA	TCC	CGG	CGC	CCT	GTT	CTT	TAT	GTT	GGC	GGT	864
5	Gly	Glu	Ser	Arg	Arg	Pro	val	Leu	Tyr	Val	Gly	Gly	
	265					270					275		
10	GCG	TGC	GCA	GCA	TCT	GGT	GAG	GAG	TTG	CGA	CGC	TTT	900
70	Ala	Cys	Ala	Ala	ser	Gly	Glu	Glu	Leu	Arg	Arg	Phe	
				280					285				
15	GTG	GAG	CTG	act	GGA	atc	CCG	GTC	ACA	act	act	CTT	936
	Val	Glu	Leu	Thr	Gly	Ile	Pro	Val	Thr	Thr	Thr	Leu	
		290					295					300	
20													
	atg	GGC	CTC	GGC	AAC	TTC	ccc	AGC	GAC	GAC	CCA	CTG	972
	Met	Gly	Leu	Gly	Asn	Phe	Pro	ser	Asp	Asp	Pro	Leu	
25					305					310			
												TAT	1008
	Ser	Leu	Arg	Met	Leu	Gly	Met		Gly	Thr	AsT	Tyr	
30			315			•		320					
									~ 5.5		555.0		9844
			TAT -										1044
35		Asn	Tyr	Ala	A91	-	гàз	WIE	asp	Leu		ren	
	325					330					335		
				~~~	000	81 M M	an m	<i>~~</i>	O C M	cmc	2 <b>~</b> 2	ccc	1080
40			GGT										7000
	ALS	Leu	Gly		Arg	Pne	ASD	ASD	345	AGT	THT	Grå	
				340					343				
45	224	2 MM	an a	COM	mmm	COB	n.c.c	n c c	G C TT	DRR	Ֆորո	GTG	1116
40			Glu										2224
	гåа		GIU	WIG	FIIG	WT 62	355	wrd	weg	<b></b>	440	360	
		350					ن ں پ						
50	000	~mm	_የ ም መ	2 <b>ខា</b> កា	ር a m	cce	<mark></mark> ሮርጥ	GRG	<i>ያ</i> ሙው	GGC	226	AAC	1152
			Asp										A & # W
	nıs	ACIT	waħ	TIG	365	£ 1.0		- W		370	- y -	2 2 TO 88	
55					555					- · ·			

	AAG	CAG	CCA	CAT	GTG	TCC	ATC	TGT	GCA	GAT	GTT	AAG	1188
	Lys	Gln	Pro	His	Val	Ser	Ile	Cys	Ala	Asp	Val	Lys	
5			375					380					
	CTT	GCT	TTG	CAG	GGC	ATG	AAT	GCT	CTT	CTT	GAA	GGA	1224
	Leu	Ala	Leu	Gln	Gly	Met	Asn	Ala	Leu	Leu	Glu	Gly	
10	385					390					395		
	AGC	ACA	TCA	AAG	AAG	AGC	TTT	GAC	TTT	GGC	TCA	TGG	1260
15	Ser	Thr	Ser	Lys	Lys	Ser	Phe	Asp	Phe	Gly	Ser	Trp	
				400					405				•
20	AAC	GAT	GAG	TTG	GAT	CAG	CAG	AAG	AGG	GAA	TTC	ccc	1296
	Asn	Asp	Glu	Leu	Asp	Gln	Gln	Lys	Arg	Glu	Phe	Pro	
		410					415					420	
25	CTT	GGG	TAT	AAA	ACA	TCT	AAT	GAG	GAG	ATC	CAG	CCA	1332
	Leu	Gly	Tyr	Lys	Thr	Ser	Asn	Glu	Glu	Ile	Gln	Pro	
					425					430			
30													
												AAA	1368
	Gln	Tyr	Ala	Ile	Gln	Val	Leu	Asp	Glu	Leu	Thr	Lys	
35			435					440					
				ATC									1404
	Gly	Glu	Ala	Ile	Ile	Gly	Thr	Gly	Val	Gly	Gln	His	
40	445					450					455		
				GCG									1440
45	Gln	Met	Trp	Ala	Ala	Gln	Tyr	Tyr	Thr	Tyr	ГÀЗ	Arg	
				460					465				
50				TGG									1476
	Pro	Arg	Gln	Trp	Leu	Ser	Ser	Ala	Gly	Leu	Gly		
		470					475					480	

	ATG	GGA	TTT	GGT	TTG	CCG	GCT	GCT	GCT	GGT	GCT	TCT	1512
	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Ala	Gly	Ala	Ser	
5					485					490			
•													
	GTG	GCC	AAC	CCA	GGT	GTT	act	GTT	GTT	GAC	atc	gat	1548
	Val	Ala	Asn	Pro	Gly	Val	Thr	Val	Val	Asp	Ile	Asp	
10			495					500					
												CTA	1584
15	Gly	Asp	Gly	Ser	Phe	Leu	Met	Asn	<b>val</b>	Gln	Glu	Leu	
	505					510					515		•
20												GTC	1620
	Ala	Met	Ile	-	Ile	Glu	ASD	Leu		AST	гÄз	AST	
				520					525				
25	en en en	an a	OM D	222	220	~~~	<b>6</b> 26	OM C	ccc	2 MC	CMC.	GTG	1656
					Asn								7020
	Lus	230	กลส	ASH	ASII	GIH	535	Ten	Grā	Mec	A 67.Y	540	
		330					<b>J</b> JJ						
30	CAG	TGG	GAG	GAC	»GG	TTC	TAT	AAG	GCC	AAC	AGA	GCG	1692
					Arg								
					545		<b>- 2</b> -	•		550	_		
35													
	CAC	ACA	TAC	TTG	GGA	AAC	CCA	GAG	AAT	GAA	agt	GAG	1728
	His	Thr	Tyr	Leu	Gly	Asn	Pro	Glu	Asn	Glu	ser	Glu	
40			555					560					
	ATA	TAT	CCA	GAT	TTC	GTG	ACG	ATC	GCC	AAA	GGG	TTC	1764
45	Ile	Tyr	Pro	Asp	Phe	Val	Thr	Ile	Ala	Lys	Gly	Phe	
	565					570					575		
50												GAA	1800
<b>50</b>	Asn	Ile	Pro	Ala	Val	Arg	<b>Val</b>	Thr	Lys	Lys	Asn	Glu	
				580					585				

	GTC	CGC	GCA	GCG	ATA	AAG	AAG	ATG	CTC	GAG	act	CCA	1836
					Ile								
_	V 42.2	590	202.43	222			595					600	
5		390											
	aaa	cca	<b>ም</b> ኤ <b>ሶ</b>	<del>ር</del> ሞር	ጥጥር	<b>ሮ</b> ልጥ	a ሞa	<b>ል</b> ጥር	<b>ሬ</b> ፕሮ	CCA	CAC	CAG	1872
													20.0
10	GTÄ	PEO	TÄE	ren	Leu	ASD	TIR	118	AGT		WYS	GIII	
					605					610			
	GAG	Cat	GTG	TTG	CCT	ATG	atc	CCT	Taa	GGT	GGG	<b>GCT</b>	1908
15	Glu	His	<b>Val</b>	Leu	Pro	Met	Ile	Pro	Asn	Gly	Gly	Ala	
			615					620					
20	TTC	AAG	gat	ATG	ATC	CTG	GAT	GGT	GAT	GGC	AGG	act	1944
	Phe	Lys	Asp	Met	Ile	Leu	Asp	Gly	Asp	Gly	Arg	Thr	
	625					630					635		
25	GTG	TAC											1950
	<b>Val</b>	Tyr											
		638											
30													
	ምር <u>አ</u> ባ	ያ <i>ፈ</i> ጥጋባ	י ממנ	<b>የ</b> ርር እ	3CAA(	3							1969
	1 GW	LOAM	mare .	CA									

	sequence ID No.: 2	
5	Sequence Type: Nucleotide and Amino Acid	
10	Sequence Length: 1969 BP's and 638 Amino Acids	
	Strandedness: Single	
15	Topology: Linear	
	Original Source Organism: Zea mays	
20	Properties: Herbicide Sensitive AHAS Enzyme	
25	AACCCTCGCG CCGCCTCCGA GACAGCCGCC GCAACC	36
	ATG GCC ACC GCC GCC GCG TCT ACC GCG CTC ACT	72
30	Met Ala Thr Ala Ala Ala Ala Ser Thr Ala Leu Thr	
	1 5 10	
	. GGC GCC ACT ACC GCT GCG CCC AAG GCG AGG CGC CGG	108
35	Gly Ala Thr Thr Ala Ala Pro Lys Ala Arg Arg Arg	100
	15 20	
40	GCG CAC CTC CTG GCC ACC CGC CGC GCC CTC GCC GCG	144
	Ala His Leu Leu Ala Thr Arg Arg Ala Leu Ala Ala	
	25 30 35	
45	000 NTO NGC MGC MGC GGG MGC GGG NTG GGG	100
	CCC ATC AGG TGC TCA GCG GCG TCA CCC GCC ATG CCG Pro Ile Arg Cys Ser Ala Ala Ser Pro Ala Met Pro	180
	40 45	
50		
	ATG GCT CCC CCG GCC ACC CCG CTC CGG CCG TGG GGC	216
	Met Ala Pro Pro Ala Thr Pro Leu Arg Pro Trp Gly	
55	50 55 60	

	ccc	ACC	GAT	CCC	CGC	AAG	GGC	GCC	GAC	ATC	CTC	GTC	252
5	Pro	Thr	Asp	Pro	Arg	rās	Gly	Ala	Asp	Ile	Leu	Val.	
					65					70			
10	GAG	TCC	CTC	GAG	CGC	TGC	GGC	GTC	CGC	GAC	GTC	TTC	288
	Glu	Ser	Leu	Glu	Arg	Суз	Gly	Asj	Arg	Asp	Asj	Phe	
			75					80					
15			ccc										324
		Tyr	Pro	Gly	Gly		Ser	Met	Glu	Ile		Gln	•
	85					90					95		
20													
												CTC	360
	Ala	Leu	Thr	_	ser	Pro	AST	ITS		asn	MIS	Leu	
25				100					105				
	mm.o	000	CAC	<i>CD C</i>	<b>4</b> 00	~~~	~a~	~~~	mmm	ccc	GCC	ጥሮሮ	396
			His										220
30	Pne	110	uis	GIU	GTII	GTÄ	115	wre	rne	wre	WTG	120	
		110					447					220	
	GGC	TAC	GCG	CGC	TCC	тсG	GGC	cgc	GTC	GGC	GTC	TGC	432
05			Ala										
35	3	- 3 -			125		•			130		-	
	ATC	GCC	ACC	TCC	GGC	ccc	GGC	GCC	ACC	AAC	CTT	GTC	468
40	Ile	Ala	Thr	Ser	Gly	Pro	Gly	Ala	Thr	Asn	Leu	Val	
			135					140					
45	TCC	GCG	CTC	GCC	GAC	GCG	CTG	CTC	gat	TCC	GTC	CCC	<b>50</b> 4
	Ser	Ala	Leu	Ala	Asp	Ala	Leu	Leu	Asp	ser	Val	Pro	
	145					150					155		
50													
	atg	GTC	GCC	ATC	ACG	GGA	CAG	GTG	CCG	CGA	CGC	ATG	540
	Met	Val	Ala	Ile	Thr	Gly	Gln	Val	Pro	Arg	Arg	Met	
ee				160					165				

5	ATT	GGC	ACC	GAC	GCC	TTC	CAG	GAG	ACG	ccc	ATC	GTC	576
	Ile	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Thr	Pro	Ile	<b>Val</b>	
		170					175					180	
10													
10	GAG	GTC	ACC	CGC	TCC	atc	ACC	AAG	CAC	AAC	TAC	CTG	612
	Glu	Val	Thr	Arg	ser	Ile	Thr	Lys	His	Asn	Tyr	Leu	
					185					190			
15													
	GTC	CTC	GAC	GTC	GAC	GAC	ATC	CCC	CGC	GTC	GTG	CAG	648
	Val	Leu	Asp	W&1	Asp	Asp	Ile	Pro	Arg	<b>val</b>	<b>Val</b>	Gln	•
20			195					200					
	GAG	GCT	TTC	TTC	CTC	GCC	TCC	TCT	GGT	CGA	CCG	GGG	684
	Glu	Ala	Phe	Phe	Leu	Ala	Ser	Ser	Gly	Arg	Pro	Gly	
25	205					210					215		
	CCG	GTG	CTT	GTC	GAC	ATC	ccc	AAG	GAC	ATC	CAG	CAG	720
30	Pro	Val	Leu	Avj	Asp	Ile	Pro	rås	Asp	Ile	Gln	Gln	
				220					225				
35	CAG	ATG	GCG	GTG	CCT	GTC	TGG	GAC	AAG	ccc	atg	agt	756
	Gln	Met	Ala	<b>Val</b>	Pro	Val	Trp	Asp	Lys	Pro	Met	Ser	
		230					235					240	
40	CTG	CCT	GGG	TAC	ATT	GCG	CGC	CTT	ccc	AAG	CCC	CCT	792
	Leu	Pro	Gly	Tyr	Ile	Ala	Arg	Leu	Pro	Lys	Pro	Pro	
					245					250			
45													
	GCG	ACT	GAG	TTG	CTT	GAG	CAG	GTG	CTG	CGT	CTT	GTT	828
	Ala	Thr	Glu	Leu	Leu	Glu	Gln	Val	Leu	Arg	Leu	Val	
50			255					260					
	GGT	GAA	TCC	CGG	CGC	CCT	GTT	CTT	TAT	GTT	GGC	GGT	864
	Gly	Glu	Ser	Arg	Arg	Pro	Val	Leu	Tyr	Val	Gly	Gly	
55	265					270					275		

	GCG	TGC	GCA	GCA	TCT	GGT	GAG	GAG	TTG	CGA	CGC	TTT	900
5	Ala	Cys	Ala	Ala	Ser	Gly	Glu	Glu	Leu	Arg	Arg	Phe	
				280					285				
10	GTG	GAG	CTG	ACT	GGA	ATC	CCG	GTC	ACA	ACT	ACT	CTT	936
	<b>Val</b>	Glu	Leu	Thr	Gly	Ile	Pro	Val	Thr	Thr	Thr	Leu	
		290					295					300	
15													
75	ATG	GGC	CTC	GGC	AAC	TTC	ccc	AGC	GAC	GAC	CCA	CTG	972
	Met	Gly	Leu	Gly	Asn	Phe	Pro	Ser	Asp	Asp	Pro	Leu	
					305					310			
20													
	TCT	CTG	CGC	ATG	CTA	GGT	ATG	CAT	GGC	ACG	GTG	TAT	1008
	Ser	Leu	Arg	Met	Leu	Gly	Met	His	Gly	Thr	Val	Tyr	
25			315					320					
	GCA	AAT	TAT	GCA	GTG	GAT	AAG	GCC	GAT	CTG	TTG	CTT	1044
30	Ala	Asn	Tyr	Ala	Val	Asp	Lys	Ala	Asp	Leu	Leu	Leu	
30	325					330					335		
	GCA	CTT	GGT	GTG	CGG	TTT	GAT	GAT	CGT	GTG	ACA	GGG	1080
35	Ala	Leu	Gly	Val	Arg	Phe	Asp	yab	Arg	Val	Thr	Gly	
				340					345				
40										AAG			1116
	Lys	Ile	Glu	Ala	Phe	Ala	Ser	Arg	Ala	Lys	Ile		
		350					355					360	
45													
												AAC	1152
	His	Val	Asp	Ile	Asp	Pro	Ala	Glu	Ile	Gly	Lys	Asn	
					365					370			
50													
												AAG	1188
•	Lys	Gln	Pro	His	Val	Ser	Ile		Ala	Asp	Val	Lys	
55			375					380					

	CTT	GCT	TTG	CAG	GGC	ATG	AAT	GCT	CTT	CTT	GAA	GGA	1224
	Leu	Ala	Leu	Gln	Gly	Met	Asn	Ala	Leu	Leu	Glu	Gly	
5	385					390					395		
	AGC	ACA	TCA	AAG	AAG	AGC	TTT	GAC	TTT	GGC	TCA	TGG	1260
	Ser	Thr	Ser	Lys	Lys	Ser	Phe	Asp	Phe	Gly	Ser	Trp	
10				400					405				
	AAC	GAT	GAG	TTG	GAT	CAG	CAG	AAG	AGG	GAA	TTC	ccc	1296
15	Asn	Asp	Glu	Leu	Asp	Gln	Gln	Lys	Arg	Glu	Phe	Pro	
		410					415					420	
20	CTT	GGG	TAT	AAA	ACA	TCT	AAT	GAG	GAG	ATC	CAG	CCA	1332
	Leu	Gly	Tyr	Lys	Thr	Ser	Asn	Glu	Glu	Ile	Gln	Pro	
					425					430			
25	CAA	TAT	GCT	ATT	CAG	GTT	CTT	GAT	GAG	CTG	ACG	AAA	1368
	Gln	Tyr	Ala	Ile	Gln	Val	Leu	Asp	Glu	Leu	Thr	Lys	
			435					440					
30													
												CAC	1404
	Gly	Glu	Ala	Ile	Ile	Gly	Thr	Gly	Val	Gly	Gln	His	
35	445					450					455		
			TGG										1440
	Gln	Met	Trp	Ala	Ala	Gln	Tyr	Tyr	Thr	Tyr	Lys	Arg	
40				460					465				
			CAG										1476
45	Pro	Arg	Gln	Trp	Leu	Ser	Ser	Ala	Gly	Leu	Gly	Ala	
		470					475					480	
50	ATG	GGA	TTT	GGT	TTG	CCG	GCT	GCT	GCT	GGT	GCT	TCT	1512
	Met	Gly	Phe	Gly	Leu	Pro	Ala	Ala	Ala	Gly	Ala	Ser	
					485					490			

	GTG	GCC	AAC	CCA	GGT	GTT	act	GTT	GTT	GAC	atc	GAT	1548
	<b>val</b>	Ala	Asn	Pro	Gly	<b>Val</b>	Thr	<b>Val</b>	Val	Asp	Ile	qea	
5			495					500					
	GGA	GAT	GGT	AGC	TTT	CTC	atg	AAC	GTT	CAG	GAG	CTA	1584
40	Gly	Asp	Gly	ser	Phe	Leu	Met	Asn	Ası	Gln	Glu	Leu	
10	505					510					515		
	GCT	atg	atc	CGA	ATT	GAG	AAC	CTC	CCG	GTG	AAG	GTC	1620
15	Ala	Met	Ile	Arg	Ile	Glu	Asn	Leu	Pro	Asj	Lys	val	•
				520					525				
20												GTG	1656
	Phe		Leu	Asn	Asn	Gln		Leu	Gly	Mot	ASI		
		530					535					540	
25													
20												GCG	1692
	Gln	Trp	Glu	Asp	_	Phe	Tyr	Lys	Ala		Arg	Ala	
					545					550			
30		5 <b>4</b> 5			<b></b>	22.0		<b></b>		<b>6</b> 555	0.65	<b>6</b> 0.6	
												GAG	1728
	HIS	Tux	Tyr	ren	GTÄ	ASN	Pro		ASI	GIW	ser	GLU	
35			555					560					
	a wa	m z m	CCA	C A M	መመረ	GMC.	B C C	2 mc	coc	aaa	ccc	መጥሮ	1764
			Pro										7/04
40	565	TYL	FLO	wab	8114	570	A 88.A	776	WYE	nys	575	2116	
	303					3,0					3.3		
	AAC	<i>ያ</i> ጥጥ	CCA	GCG	GTC	CGT	GTG	ACA	AAG	AAG	AAC	GAA	1800
45			Pro										
45				580		5			585			-50	
	GTC	CGC	GCA	GCG	ATA	AAG	AAG	ATG	CTC	GAG	act	CCA	1836
50			Ala										<b>~</b>
		590	<del>-</del>			-2-	595				<b></b>	600	

	GGG	CCG	TAC	CTC	TTG	GAT	ATA	ATC	GTC	CCA	CAC	CAG	1872
	Gly	Pro	Tyr	Leu	Leu	Asp	Ile	Ile	<b>Val</b>	Pro	His	Gln	
5					605					610			
												GCT	1908
10	Glu	His		Leu	Pro	ret	Ile		r98	Gly	GIA	Ala	
			615					620					
	ሙጥረ	BBG	ሮ <i>ክ</i> ጥ	<del>አ</del> ሞሮ	a ጥር	ርሞር	ሮ ^გ ጥ	ርርጥ	ር <mark>አ</mark> ጥ	ccc	agg	act	<b>19</b> 44
15												Thr	
	625	- <u>7</u> -				630	<u>F</u>	1		2	635		
				•									
20	GTG	TAC											1950
	Val	Tyr											
		638											
25													
	TGAT	CTAI	. AAA	rccac	GCAA(	3							1969
30													
35													
00													
40													
40													
			•										
45													
50												•	
55													

	Sequence ID No.: 3	
5	Sequence Type: Nucleotide and Amino Acid	
10	Sequence Length: 1969 BP's and 638 Amino Acids	
	Strandedness: Single	
15	Topology: Linear	
	Original Source Organism: Zea mays	
20	Properties: Herbicide Sensitive AHAS Enzyme	
25	AACCCTCGCG CCGCCTCCGA GACAGCCGCC GCAACC	36
20	AACCCTCGCG CCGCCTCCGA GACAGCCGCC GCAACC	36
	ATG GCC ACC GCC GCC GCG TCT ACC GCG CTC ACT	72
30	Met Ala Thr Ala Ala Ala Ala Ser Thr Ala Leu Thr	
	1 5 10	
	GGC GCC ACT ACC GCT GCG CCC AAG GCG AGG CGC CGG	108
35	Gly Ala Thr Thr Ala Ala Pro Lys Ala Arg Arg Arg	
	15 20	
40	GCG CAC CTC CTG GCC ACC CGC CGC GCC CTC GCC GCG	144
	Ala His Leu Leu Ala Thr Arg Arg Ala Leu Ala Ala	
	25 30 35	
45	CCC ATC AGG TGC TCA GCG GCG TCA CCC GCC ATG CCG	180
	Pro Ile Arg Cys Ser Ala Ala Ser Pro Ala Met Pro	100
	40 45	
50		
	ATG GCT CCC CCG GCC ACC CCG CTC CGG CCG TGG GGC	216
	Met Ala Pro Pro Ala Thr Pro Leu Arg Pro Trp Gly	
55	50 55 60	

	CCC	ACC	GAG	ccc	CGC	AAG	GGT	GCT	GAC	atc	CTC	GTC	252
5	Pro	Thr	Glu	Pro	Arg	Lys	Gly	Ala	Asp	Ile	Leu	<b>A</b> 57	
					65					70			
10	GAG	TCC	CTC	GAG	CGC	TGC	GGC	GTC	CGC	GAC	GTC	TTC	288
	Glu	ser	Leu	Glu	Arg	Cys	Gly	ASI	Arg	Asp	Asj	Phe	
			75					80					
15	000	MD A	000	CCC	cco	coc	MAA	2000	GAG	2 MA	020	CR C	324
									Glu				364
	85	~ ¥ ~	FLU	GLY	G _Z y	90	DCI	Mec	G 7 60	226	95	924	
	00												
20	GCA	CTC	ACC	CGC	TCC	ccc	GTC	ATC	GCC	AAC	CAC	CTC	360
	Ala	Leu	Thr	Arg	Ser	Pro	va1	Ile	Ala	Asn	His	Leu	
				100					105				
25												•	
	TTC	CGC	CAC	GAG	CAA	GGG	GAG	GCC	TTT	GCC	GCC	TCC	396
	Phe	Arg	His	Glu	Gln	Gly	Glu	Ala	Phe	Ala	Ala	Ser	
30		110					115					120	
	GGC	TAC	GCG	CGC	TCC	TCG	GGC	CGC	GTC	GGC	GTC	TGC	432
35	Gly	Tyr	Ala	Arg	Ser	Ser	Gly	Arg	<b>Val</b>	Gly	A97	Cys	
					125					130			
40									ACC				468
	Ile	Ala		Ser	Gly	Pro	Gly		Thr	ASN	Leu	AST	
			135					140					
45	ጥሮሮ	GCG	CTC	GCC	GAC	GCG	ርጥਫ	CTC	GAT	TCC	GTC	CCC	<b>50</b> 4
									Asp				
	145					150					155		
50	ATG	GTC	GCC	ATC	ACG	GGA	CAG	GTG	CCG	CGA	CGC	ATG	540
									Pro				
				160		-			165	-	-		
55													

	ATT	GGC	ACC	GAC	GCC	TTC	CAG	GAG	ACG	CCC	ATC	GTC	576
	Trp	Gly	Thr	Asp	Ala	Phe	Gln	Glu	Thr	Pro	Ile	AUI	
5		170					175					180	
									_			CTG	612
10	Glu	Val	Thr	Arg		Ile	Thr	räs	His		Tyr	Leu	
70					185					190			
	GTC	CTC	GAC	GTC	GAC	GAC	ATC	CCC	CGC	GTC	GTG	CAG	648
15	<b>Val</b>	Leu	Asp	<b>Val</b>	Asp	Asp	Ile	Pro	Arg	Asj	val	Gln	•
			195					200					
20	GAG	GCT	TTC	TTC	CTC	GCC	TCC	TCT	GGT	CGA	CCA	GGG	684
20	Glu	Ala	Phe	Phe	Leu	Ala	Ser	8er	Gly	Arg	Pro	Gly	
	205					210					215		
25	CCG	GTG	CTT	GTC	GAC	ATC	ccc	AAG	GAC	atc	CAG	CAG	720
	Pro	va1	Leu	Wal	Asp	Ile	Pro	Lys	Asp	Ile	Gln	Gln	
				220					225				
30													
	CAG	ATG	GCG	GTG	CCT	GTC	TGG	GAC	AAG	CCC	ATG	agt	756
	Gln	Met	Ala	val	Pro	val	Trp	Asp	Lys	Pro	Met	ser	
35		230					235		•			240	
			GGG										792
	Leu	Pro	Gly	Tyr	Ile	Ala	Arg	Leu	Pro	Lys	Pro	Pro	
40					245					250			
			GAG										828
45	Ala	Thr	Glu	Leu	Leu	Glu	Gln		Leu	Arg	Leu	A91	
			255					260					
													_ = .
50			TCG										864
	_	Glu	Ser	Arg	Arg		Val	Leu	Tyr	Val	_	Gly	
	265					270					275		

	GCG	TGC	GCA	GCA	TCT	GGT	GAG	GAG	TTG	CGA	CGC	TTT	900
	Ala	Cys	Ala	Ala	Ser	Gly	Glu	Glu	Leu	Arg	Arg	Phe	
5				280					285				
	GTG	GAG	CTG	ACT	GGA	ATC	CCG	GTC	ACA	ACT	ACT	CTT	936
	Val	Glu	Leu	Thr	Gly	Ile	Pro	Val	Thr	Thr	Thr	Leu	
10		290					295					300	
	ATG	GGC	CTC	GGC	AAC	TTC	ccc	AGC	GAC	GAC	CCA	CTG	972
15	Met	Gly	Leu	Gly	Asn	Phe	Pro	Ser	Asp	Asp	Pro	Leu	
					305					310			•
20	TCT	CTG	CGC	ATG	CTA	GGT	ATG	CAT	GGG	ACG	GTG	TAT	1008
	Ser	Leu	Arg	Met	Leu	Gly	Met	His	Gly	Thr	Val	Tyr	
			315					320					
25	GCA	AAT	TAT	GCA	GTG	GAT	AAG	GCC	GAT	CTG	TTG	CTT	1044
	Ala	Asn	Tyr	Ala	Val	Asp	Lys	Ala	Asp	Leu	Leu	Leu	
	325					330					335		
30													
	GCA	CTT	GGT	GTG	CGG	TTT	GAT	GAT	CGT	GTG	ACA	GGG	1080
	Ala	Leu	Gly	Val	Arg	Phe	Asp	Asp	Arg	Val	Thr	Gly	
35				340					345				
	AAG	ATT	GAG	GCT	TTT	GCA	AGC	AGG	GCT	AAG	ATT	GTG	1116
	Lys	Ile	Glu	Ala	Phe	Ala	Ser	Arg	Ala	Lys	Ile	Val	
40		350					355					360	
	CAC	GTT	GAT	ATT	GAT	CCG	GCT	GAG	ATT	GGC	AAG	AAC	1152
45	His	Val	Asp	Ile	Asp	Pro	Ala	Glu	Ile	Gly	Lys	Asn	
					365					370			
50	AAG	CAG	CCA	CAT	GTG	TCC	ATC	TGT	GCA	GAT	GTT	AAG	1188
	Lys	Gln	Pro	His	Val	Ser	Ile	Cys	Ala	Asp	Val	Lys	
			375					380					

	CTT	GCT	TTG	CAG	GGC	ATG	AAT	GCT	CTT	CTT	GAA	GGA	1224
	Leu	Ala	Leu	Gln	Gly	Met	Asn	Ala	Leu	Leu	Glu	Gly	
5	385					390					395		
	AGC	ACA	TCA	aag	AAG	AGC	TTT	GAC	TTT	GGC	TCA	TGG	1260
10	Ser	Thr	ser	Lys	Lys	ser	Phe	Asp	Phe	Gly	8er	Trp	
70				400					405				
	AAC	GAT	GAG	TTG	gat	CAG	CAG	AAG	AGG	Gaa	TTC	CCC	1296
15	Asn	Asp	Glu	Leu	asp	Gln	Gln	Lys	Arg	Glu	Phe	Pro	
		410					415					420	
20	CTT	GGG	TAT	AAA	ACA	TCT	AAT	GAG	GAG	atc	CAG	CCA	1332
	Leu	Gly	Tyr	Lys	Thr	Ser	Asn	Glu	Glu	Ile	Gln	Pro	
					425					430			
25													
												AAA	1368
	Gln	Tyr		Ile	Gln	val	Leu	_	Glu	Leu	Thr	Lys	
••			435					440					
30													
												CAC	1404
	_	Glu	WIE	118	118	_	TNY	GTÅ	AST	СТĀ	Gln	HIS	
35	445					450					455		
	O2 M	2 M.C	mcc	ccc	COR	OB C	m z 🗢	Ma ~	2 Cm	<i>የተያ</i>	AAG	ccc	1440
													2010
40	GTII	Met	TTD	460	WTO	GIM	* <b>X</b> *	~ X ~	465	~ 7 ~	Lys	mra	
				400					203				
	CCB	a.cc	CAG	ጥሮር	ጥጥር	ጥርጥ	тса	GCT	GGT	CTT	GGG	GCT	1476
45											Gly		
		470		225	200		475				1	480	
		<b>11,7</b> ♥											
	ልጥሮ	GGA	ጥጥጥ	GGT	ттс	CCG	GCT	GCT	GCT	GGT	GCT	TCT	1512
50											Ala		
		1		1	485					490			

5	GTG	GCC	AAC	CCA	GGT	GTC	ACT	GTT	GTT	GAC	ATC	GAT	1548
v	Val	Ala	Asn	Pro	Gly	Val	Thr	val	<b>v</b> el	Asp	Ile	Asp	
			495					500					
10	GGA	GAT	GGT	AGC	TTT	CTC	atg	AAC	GTT	CAG	GAG	CTA	1584
	Gly	Asp	Gly	Ser	Phe	Leu	ret	Asn	<b>Val</b>	Gln	Glu	Leu	
	505					510					515		
15													
	GCT	atg	atc	CGA	ATT	GAG	AAC	CTC	CCA	GTG	AAG	GTC	1620
	Ala	Met	Ile	Arg	Ile	Glu	Asn	Leu	Pro	Asj	rās	<b>V21</b>	
20				520					525				
	TTT	GTG	CTA	AAC	AAC	CAG	CAC	CTG	GGG	ATG	GTG	GTG	1656
a-	Phe	Val	Leu	Asn	Asn	Gln	His	Leu	Gly	Met	Val	Val	
25		530					535					540	
												GCG	1692
30	Gln	Trp	Glu	Asp	_	Phe	Tyr	Lys	Ala		Arg	Ala	
					545					550			
					<b>88</b> 5	22.0	<b>~~</b>	<b>~</b> 5~	0.069	<b>4</b> 00	5.45	<b>4</b> 5.4	9700
35												GAG	1728
	nis	Tur	Tyr 555	nen	GIY	ASII	b to	560	ASI	GLU	PAT	GLU	
			333					300					
40	a ma	יוף בעיף	CCA	ር ኤ ጥ	ጥጥሮ	GTG	»cc	^ኤ ሞሮ	GCC	28.28	GGG	ጥጥር	1764
			Pro										2.00
	565	* X *	***	wos		570	2 86 2		2526	ک پرت	575		
4.5	303												
45	AAC	ATT	CCA	GCG	GTC	CGT	GTG	ACA	AAG	AAG	AAC	GAA	1800
			Pro										
				580		•			585	- <b>-</b>			
50													
	GTC	CGC	GCA	GCG	ATA	AAG	AAG	ATG	CTC	GAG	ACT	CCA	1836
			Ala										
55		590				-	595					600	

	GGG	CCG	TAC	CTC	TTG	GAT	ATA	ATC	GTC	CCA	CAC	CAG	1872
5	Gly	Pro	Tyr	Leu	Leu	Asp	Ile	Ile	<b>Val</b>	Pro	His	Gln	
					605					610			
10	GAG	CAT	GTG	TTG	CCT	ATG	ATC	CCT	agt	GGT	GGG	GCT	1908
70	Glu	His	Val	Leu	Pro	Met	Ile	Pro	ser	Gly	Gly	Ala	
			615					620					
15	TTC	AAG	gat	atg	ATC	CTG	GAT	GGT	gat	GGC	AGG	act	<b>19</b> 44
	Phe	Lys	Asp	Met	Ile	Leu	Asp	Gly	Asp	Gly	Arg	Thr	
	625					630					635		•
20													
	GTG	TAC											1950
	<b>val</b>	Tyr											
		638											
25													
	TGAT	CTAI	AAA 1	CCAC	CAAC	3							1969

Claims

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1. A monocot nucleic acid sequence encoding a functional AHAS enzyme, which enzyme has an amino acid substitution relative to a wild-type monocot AHAS enzyme, and which substitution confers

- 2. The sequence of Claim 1 in which the monocot is corn and the substitution is at position 621 in the wild-type corn AHAS enzyme.
- 3. The sequence of Claim 2 in which the substituted amino acid is asparagine.
- 4. A functional monocot AHAS enzyme which has an amino acid substitution relative to a monocot wild-type AHAS enzyme, and which substitution confers imidazolinone-specific resistance to the enzyme.
- 5. The enzyme of Claim 4 in which the monocot is corn and the substitution is at position 621 in the wild-type corn AHAS enzyme.
- 6. The enzyme of Claim 5 in which the substituted amino acid is asparagine.
- 7. A transformation vector comprising the nucleic acid of Claim 1.

imidazolinone-specific resistance to the enzyme.

- 8. A host cell comprising the nucleic acid sequence of Claim 1, or the vector of Claim 7.
- 55 9. The host cell of Claim 8 which is a plant cell or a bacterial cell.
  - 10. An imidazolinone-specific resistant mature plant containing the nucleic acid sequence of Claim 1, or seed or pollen therefrom.

- 11. A method of conferring imidazolinone-specific resistance to a plant cell which comprises providing the plant cell with the nucleic acid sequence of Claim 1.
- 12. A method for growing imidazolinone-specific resistant plants which comprises cultivating a plant which produces the enzyme of Claim 4 in the presence of an inhibitory amount of imidazolinone.
  - 13. A method of selecting host cells successfully transformed with a gene of interest which comprises providing to prospective host cells the gene of interest linked to the nucleic acid sequence of Claim 1, or unlinked but in the presence of the nucleic acid sequence of Claim 1, growing the cells in the presence of an inhibitory amount of imidazolinone and identifying surviving cells as containing the gene of interest.
  - 14. A nucleic acid construct comprising the sequence of Claim 1 linked to a gene encoding an agronomically useful trait.

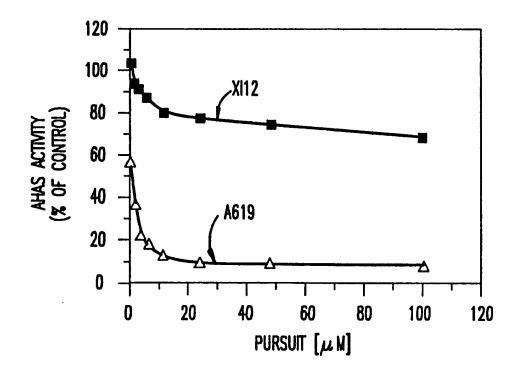


FIG.1A

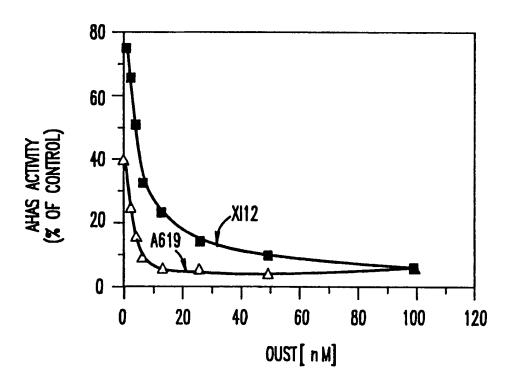
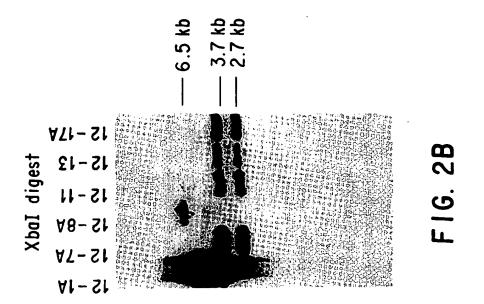
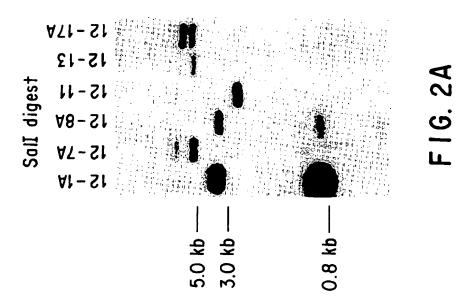


FIG.1B





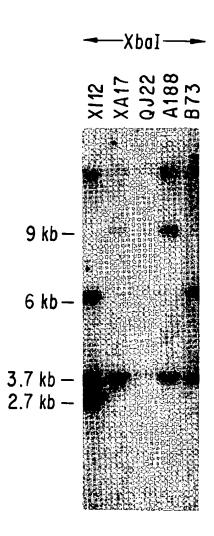
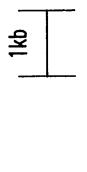
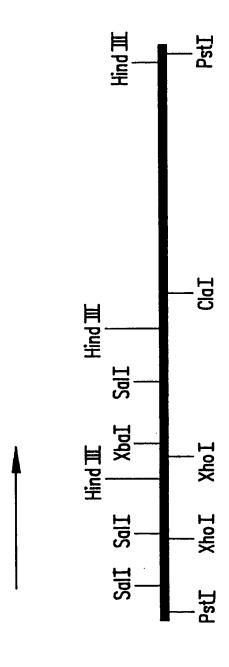


FIG. 3





-16.4

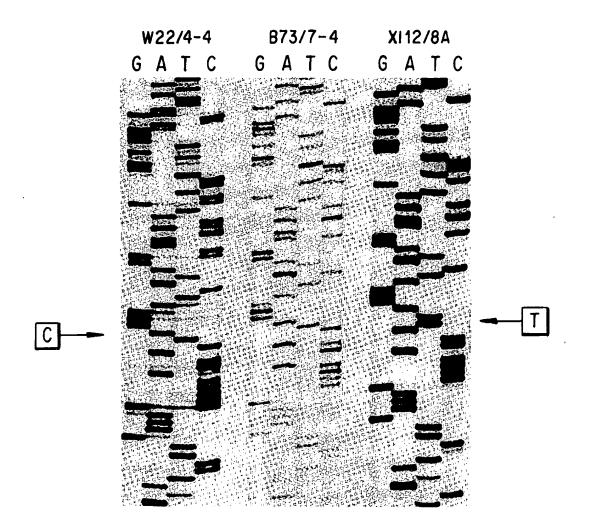


FIG. 5A

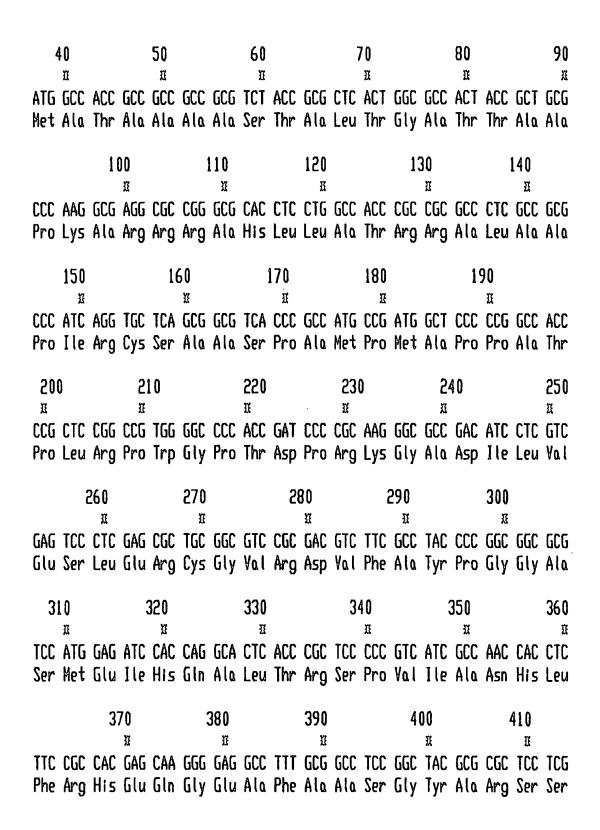
W22/1A and B73/7-4 sequence:

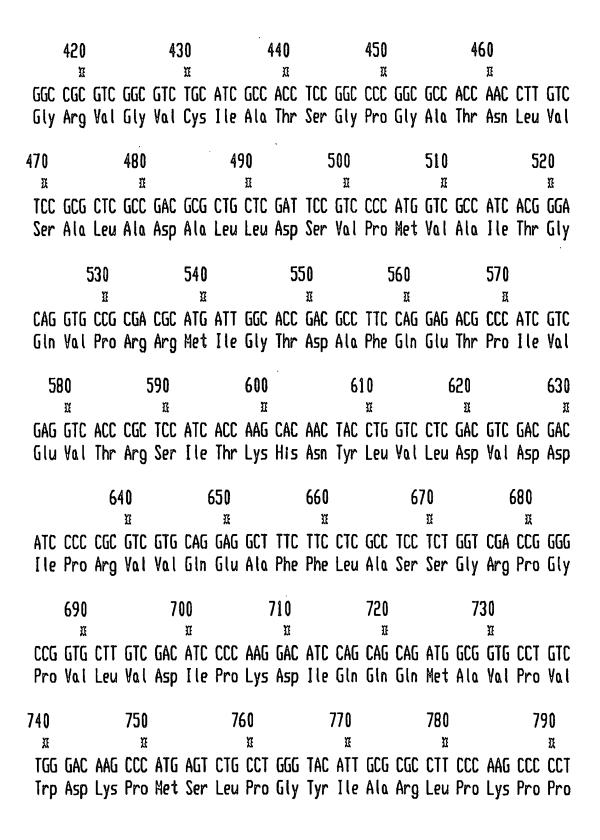
5'TAGTG3' 3'ATCTG5'

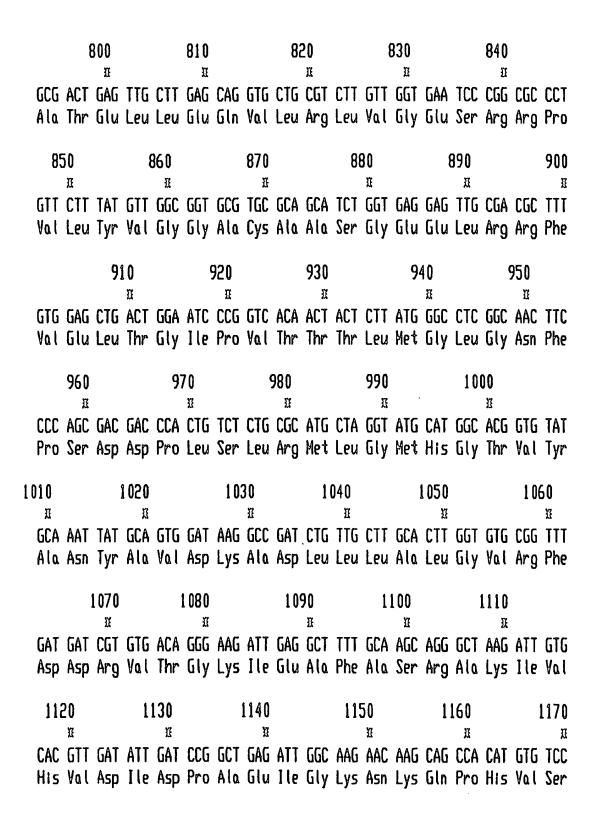
XI12/8A sequence:

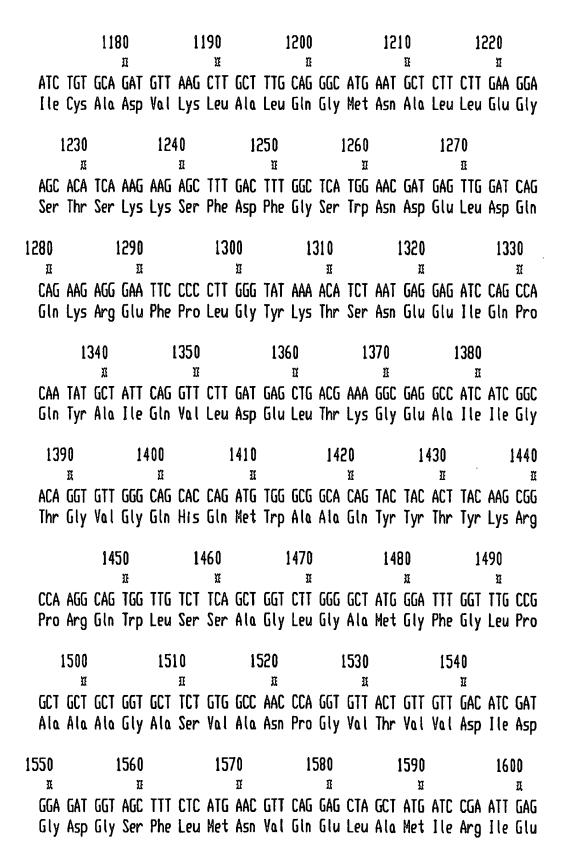
5'TAATG3' 3'ATTAC5'

F1G. 5B









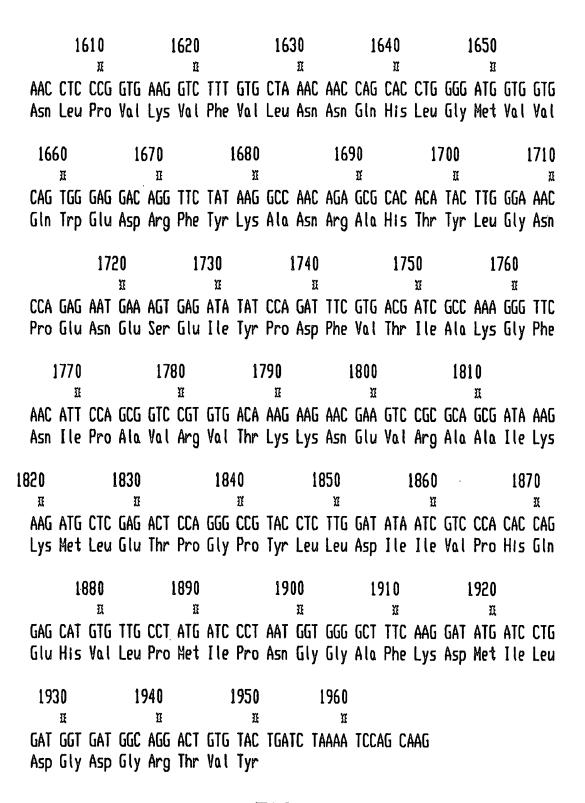


FIG.6E

W740/04	44000	10		20		30	50	40		50		60
X112/8A	AACCC	ICGCG	CCGCC	TCCGA	GACAG	CCGCC	GCAAC	CATGG	CCACC	GCCGC	CGCCG	CGTCT
A55/19				TCCGA								
				11111								
B73/7-4				TCCGA								
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
X112/8A	AACCC	TCGCG	CCGCC	TCCGA	GACAG	CCGCC	GCAAC	CATGG	CCACC	GCCGC	CGCCG	CGTCT
		70		80		90		100		110		120
XI12/8A	ACCGC	GCTCA	CTGGC	GCCAC	TACCG	CTGCG	СССАА	GGCGA	rece	רנינינ	<b>GLACE</b>	TOOTE
	110000	COTON	01000	000110	711000	0,000	COUNT	ddbdii	docat	Coude	UCHCC	10010
H55\1V	ACCGC	GCTCA	CTGGC	GCCAC	TACCG	CTGCG	CCCAA	GGCGA	GGCGC	CGGGC	GCACC	TCCTG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4	ACCGC	GCTCA	CTGGC	GCCAC	TACCG	CTGCG	CCCAA	GGCGA	GGCGC	CGGGC	GCACC	TCCTG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
XI12/8A												
		130		140		150		160		170		180
XI12/8A	GCCAC	CCGCC	GCGCC	CTCGC	CCCCC	CCATC	AGGTG	CTCAG	CGGCG	TCACC	CGCCA	TGCCG
A55/19				CTCGC								
				11111								
B73/7-4	GCCAC	CCGCC	GCGCC	CTCGC	CGCGC	CCATC	AGGTG	CTCAG	CGGCG	TCACC	CGCCA	TGCCG
				11111								
XI15/84	GCCAC	CCGCC	GCGCC	CTCGC	CGCGC	CCATC	AGGTG	CTCAG	CGGCG	TCACC	CGCCA	TGCCG
		190		200		210		550		530		240
X115/89	ATUGC	ICCCC	CGGCC	ACCCC	GCTCC	GGCCG	TGGGG	CCCCA	CCGAT	CCCCG	CAAGG	GCGCC
¥22/1A	ATGGC	TCCCC	Րեւ	ΔΓΓΓΓ	GCTCC	הנוננ	TGGGG	LLLLV	TAJO	נררני	ראאנינ	י /
466/ III				11111								
B73/7-4	אדההר	TUUUL	וונונ	VLLLL	נוזוו	ווווו	TEEEE	LLLLV	CCCV~	11111	CAACC	C+Co+
1 ווטוע	11111	11111	11111	11111	11111	11111	11111	11111	IIII	11111	11111	1 11
XI12/8A												
אט/כווץ	ATEEL	1rrrr	reer	<b>VLLLL</b>	COTOO	CCCCC	TCCCC	CCCCA	CCCAT	CCCCC	CAACC	CCCCC

VI 10 /0A	CAPAT	250	TOTAG			270		580 580	ልቦርፓቦ		רדארר	300
XI12/8A	UALAI	LLILU	ICUNU	16661	CUNUC	UCTUC	uucui	ccucu	ncuic	TTCUC	CINCC	CCUUC
H22/1A								CCGCG				
								11111				
B73/7-4								CCGCG				
XI12/8A								11111 CCGCG				
ALIC/OH	UNCHI	CCTCU	Lunu	16661	CUHUC	06106	uucui	CCUCU	пситс	11000	CINCO	CCUUC
		310		320		330		340		350		360
XI12/8A	GGCGC	GTCCA	TGGAG	ATCCA	CCAGG	CACTC	ACCCG	CTCCC	CCGTC	ATCGC	CAACC	ACCTC
1100 /1 4	rcere	CTCCA	TCCAC	ATCCA	רראנר	CACTC	YCCCL.	CTCCC	ררנדר	ATCCC	CYVCC	ΑΓΓΤΓ
A55/19								CTCCC 11111				
XB73/7-4								CTCCC				
,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,,								11111				
XI12/8A	GGCGC	GTCCA	TGGAG	ATCCA	CCAGG	CACTC	ACCCG	CTCCC	CCGTC	ATCGC	CAACC	ACCTC
		270		201		201		400		410		AON
Y112/QA	TTCC	370 crace						400 CGGCT				420 50000
X112/8A	TTCCG							400 CGGCT				
X112/8A V22/1A		CCACG	AGCAA	GGGGA	GGCCT	TTGCG >	GCCTC		ACGCG	CGCTC	CTCGG	GCCGC
W22/1A	TTCCG 11111	CCACG CCACG 11111	AGCAA 11111	GGGGA 11111	GGCCT 11111	TTGCG > TTGCG	GCCTC GCCTC 11111	CGGCT CGGCT 11111	ACGCG ACGCG 11111	CGCTC CGCTC 11111	CTCGG 11111	GCCGC 11111
	TTCCG 11111 TTCCG	CCACG CCACG 11111 CCACG	AGCAA 11111 AGCAA	GGGGA GGGGA 11111 GGGGA	GGCCT 11111 GGCCT	TTGCG  TTGCG L111 TTGCc	GCCTC GCCTC 11111 GCCTC	CGGCT CGGCT 11111 CGGCT	ACGCG 11111 ACGCG	CGCTC 11111 CGCTC	CTCGG 11111 CTCGG	GCCGC GCCGC 11111 GCCGC
W22/1A B73/7-4	TTCCG 11111 TTCCG 11111	CCACG 11111 CCACG 11111	AGCAA 11111 AGCAA 11111	GGGGA 11111 GGGGA 11111	GGCCT 11111 GGCCT 11111	TTGCG	GCCTC GCCTC 11111 GCCTC 11111	CGGCT 11111 CGGCT 11111	ACGCG 11111 ACGCG 11111	CGCTC 11111 CGCTC 11111	CTCGG 11111 CTCGG 11111	GCCGC GCCGC 11111 GCCGC 11111
W22/1A	TTCCG 11111 TTCCG 11111	CCACG 11111 CCACG 11111	AGCAA 11111 AGCAA 11111	GGGGA 11111 GGGGA 11111	GGCCT 11111 GGCCT 11111	TTGCG	GCCTC GCCTC 11111 GCCTC 11111	CGGCT CGGCT 11111 CGGCT	ACGCG 11111 ACGCG 11111	CGCTC 11111 CGCTC 11111	CTCGG 11111 CTCGG 11111	GCCGC GCCGC 11111 GCCGC 11111
W22/1A B73/7-4 XI12/8A	TTCCG 11111 TTCCG 11111 TTCCG	CCACG 11111 CCACG 11111 CCACG 430	AGCAA 11111 AGCAA 11111 AGCAA	GGGGA 11111 GGGGA 11111 GGGGA 440	GGCCT 11111 GGCCT 11111 GGCCT	TTGCG	GCCTC 11111 GCCTC 11111 GCCTC	CGGCT 11111 CGGCT 11111 CGGCT 460	ACGCG 11111 ACGCG 11111 ACGCG	CGCTC 11111 CGCTC 11111 CGCTC 11111 CGCTC 470	CTCGG 11111 CTCGG 11111 CTCGG	GCCGC GCCGC 11111 GCCGC 11111 GCCGC
W22/1A B73/7-4	TTCCG 11111 TTCCG 11111 TTCCG	CCACG 11111 CCACG 11111 CCACG 430	AGCAA 11111 AGCAA 11111 AGCAA	GGGGA 11111 GGGGA 11111 GGGGA 440	GGCCT 11111 GGCCT 11111 GGCCT	TTGCG	GCCTC 11111 GCCTC 11111 GCCTC	CGGCT 11111 CGGCT 11111 CGGCT 460	ACGCG 11111 ACGCG 11111 ACGCG	CGCTC 11111 CGCTC 11111 CGCTC 11111 CGCTC 470	CTCGG 11111 CTCGG 11111 CTCGG	GCCGC GCCGC 11111 GCCGC 11111 GCCGC
W22/1A B73/7-4 XI12/8A XI12/8A	TTCCG 11111 TTCCG 11111 TTCCG	CCACG 11111 CCACG 11111 CCACG 430 CGTCT	AGCAA 11111 AGCAA 11111 AGCAA GCAA	GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC	GGCCT 11111 GGCCT 11111 GGCCT CTCCG	TTGCG  TTGCG  1111  TTGCC  1111  TTGCG  450  GCCCC	GCCTC 11111 GCCTC 11111 GCCTC GGCGC	CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA	ACGCG 11111 ACGCG 11111 ACGCG ACGCTT	CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC	CTCGG 11111 CTCGG 11111 CTCGG	GCCGC GCCGC 11111 GCCGC 11111 GCCGC 480 TCGCC
W22/1A B73/7-4 XI12/8A	TTCCG 11111 TTCCG 11111 TTCCG GTCGG	CCACG CCACG 11111 CCACG 11111 CCACG 430 CGTCT	AGCAA AGCAA 11111 AGCAA 11111 AGCAA GCATC	GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC	GGCCT GGCCT HIHI GGCCT HIHI GGCCT CTCCG	TTGCG  TTGCG  1111 TTGCC  1111 TTGCG  450 GCCCC	GCCTC GCCTC 11111 GCCTC 11111 GCCTC GGCGC	CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA	ACGCG 11111 ACGCG 11111 ACGCG ACCTT ACCTT	CGCTC CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC	CTCGG 11111 CTCGG 11111 CTCGG CGCGC	GCCGC GCCGC H1111 GCCGC H1111 GCCGC 480 TCGCC TCGCC
W22/1A B73/7-4 XI12/8A XI12/8A W22/1A	TTCCG 11111 TTCCG 11111 TTCCG 6TCGG 6TCGG 11111	CCACG 11111 CCACG 11111 CCACG 430 CGTCT 11111	AGCAA 11111 AGCAA 11111 AGCAA GCATC GCATC 11111	GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC GCCAC	GGCCT 11111 GGCCT 11111 GGCCT CTCCG CTCCG 11111	TTGCG	GCCTC 11111 GCCTC 11111 GCCTC GGCGC GGCGC 11111	CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA CACCA	ACGCG 11111 ACGCG 11111 ACGCG ACGCTT ACCTT 1111	CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC GTCTC 11111	CTCGG 11111 CTCGG 11111 CTCGG CTCGG 11111 CTCGG	GCCGC GCCGC H1111 GCCGC H1111 GCCGC 480 TCGCC TCGCC
W22/1A B73/7-4 XI12/8A XI12/8A	TTCCG 11111 TTCCG 11111 TTCCG 6TCGG 11111 GTCGG	CCACG 11111 CCACG 11111 CCACG 11111 CCACG 430 CGTCT 11111 CGTCT	AGCAA 11111 AGCAA 11111 AGCAA GCATC GCATC 11111 GCATC	GGGGA 11111 GGGGA 11111 GGGGA 440 GCCAC GCCAC 11111 GCCAC	GGCCT GGCCT HIHI GGCCT CTCCG CTCCG HIHI CTCCG	TTGCG  TTGCG  1111  TTGCC  1111  TTGCG  450  GCCCC  11111  GCCCC	GCCTC 11111 GCCTC 11111 GCCTC GGCGC GGCGC 111111 GGCGC	CGGCT 11111 CGGCT 11111 CGGCT 460 CACCA	ACGCG 11111 ACGCG 11111 ACGCG ACCTT ACCTT 1111 ACCTG	CGCTC 11111 CGCTC 11111 CGCTC 470 GTCTC 11111 GTCTC	CTCGG 11111 CTCGG 11111 CTCGG CTCGG 11111 CTCGG	GCCGC  GCCGC  11111 GCCGC  11111 GCCGC  480 TCGCC  TCGCC  11111 TCGCC

		490		500		510		520		530		540
XI12/8A	GACGC	GCTGC	TCGAT	TCCGT	CCCCA	TGGTC	GCCAT	CACGG	GACAG	GTGCC	GCGAC	GCATG
422/1A	GACGC	GCTGC	TCGAT	TCCGT	CCCCA	TGGTC	GCCAT	CACGG	GACAG	GTGCC	GCGAC	GCATG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4				TCCGT								
				11111								
XI12/8A	GACGC	GCTGC	TCGAT	TCCGT	CCCCA	TGGTC	GCCAT	CACGG	GACAG	GTGCC	GCGAC	GCATG
		<i></i>		<b>5</b> / <b>0</b>		<b>-7</b> 0		500		F00		
V710/01	ATTCC			560								
X115/89	Alluu	CACLU	ALULL	TTCCA	UUAUA	Lulll	AILUI	LUAUU	ILALL	しいしまし	LAILA	CLAAG
422/1A	ATTGG	LACCE	ልቦቤቦቦ	TTCCA	<u> </u>	CECCC	ATCGT	ՐԱԳԱ	TOACE	CECTC	ΔΊΤΑ	CCAAG
WEE/ IN				11111								
B73/7-4				TTCCA								
<b>3.3.7.</b> V				11111								
XI12/8A				TTCCA								
				620								
XI12/8A	CACAA			620 CTCGA								
		CTACC	TGGTC	CTCGA	CGTCG	ACGAC	ATCCC	CCGCG	TCGTG	CAGGA	GGCTT	TCTTC
XI12/8A Y22/1A	CACAA	CTACC CTACC	TGGTC TGGTC	CTCGA CTCGA	CGTCG CGTCG	ACGAC ACGAC	ATCCC ATCCC	CCGCG	TCGTG TCGTG	CAGGA CAGGA	GGCTT GGCTT	TCTTC TCTTC
¥22/1A	CACAA 11111	CTACC CTACC 11111	TGGTC TGGTC 11111	CTCGA CTCGA 11111	CGTCG CGTCG 11111	ACGAC 11111	ATCCC 11111	CCGCG 11111	TCGTG TCGTG 11111	CAGGA CAGGA 11111	GGCTT GGCTT 11111	TCTTC 11111
	CACAA 11111 CACAA	CTACC CTACC 11111 CTACC	TGGTC 11111 TGGTC	CTCGA CTCGA 11111 CTCGA	CGTCG CGTCG 11111 CGTCG	ACGAC 11111 ACGAC	ATCCC 11111 ATCCC	CCGCG 11111 CCGCG	TCGTG TCGTG 11111 TCGTG	CAGGA CAGGA 11111 CAGGA	GGCTT 11111 GGCTT	TCTTC TCTTC 11111 TCTTC
¥22/1A B73/7-4	CACAA 11111 CACAA 11111	CTACC 11111 CTACC 11111	TGGTC 11111 TGGTC 11111	CTCGA CTCGA 11111 CTCGA 11111	CGTCG CGTCG 11111 CGTCG 11111	ACGAC 11111 ACGAC 11111	ATCCC 11111 ATCCC 11111	CCGCG 11111 CCGCG 11111	TCGTG TCGTG 11111 TCGTG 11111	CAGGA CAGGA 11111 CAGGA 11111	GGCTT 11111 GGCTT 11111	TCTTC TCTTC 11111 TCTTC 11111
¥22/1A	CACAA 11111 CACAA 11111	CTACC 11111 CTACC 11111	TGGTC 11111 TGGTC 11111	CTCGA CTCGA 11111 CTCGA	CGTCG CGTCG 11111 CGTCG 11111	ACGAC 11111 ACGAC 11111	ATCCC 11111 ATCCC 11111	CCGCG 11111 CCGCG 11111	TCGTG TCGTG 11111 TCGTG 11111	CAGGA CAGGA 11111 CAGGA 11111	GGCTT 11111 GGCTT 11111	TCTTC TCTTC 11111 TCTTC 11111
¥22/1A B73/7-4	CACAA 11111 CACAA 11111	CTACC 11111 CTACC 11111 CTACC	TGGTC 11111 TGGTC 11111 TGGTC	CTCGA CTCGA 11111 CTCGA 11111 CTCGA	CGTCG 11111 CGTCG 11111 CGTCG	ACGAC 11111 ACGAC 11111 ACGAC	ATCCC 11111 ATCCC 11111 ATCCC	CCGCG 11111 CCGCG 11111 CCGCG	TCGTG TCGTG 11111 TCGTG 11111 TCGTG	CAGGA 11111 CAGGA 11111 CAGGA CAGGA	GGCTT 11111 GGCTT 11111 GGCTT 11111 GGCTT	TCTTC 11111 TCTTC 11111 TCTTC
¥22/1A B73/7-4 XI12/8A	CACAA 11111 CACAA 11111 CACAA	CTACC 11111 CTACC 11111 CTACC 11111 CTACC	TGGTC TGGTC 11111 TGGTC 11111 TGGTC	CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680	CGTCG CGTCG 11111 CGTCG 11111 CGTCG	ACGAC 11111 ACGAC 11111 ACGAC 690	ATCCC 11111 ATCCC 11111 ATCCC	CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700	TCGTG TCGTG 11111 TCGTG 11111 TCGTG	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 710	GGCTT 11111 GGCTT 11111 GGCTT	TCTTC 11111 TCTTC 11111 TCTTC 11111 TCTTC 720
¥22/1A B73/7-4	CACAA 11111 CACAA 11111 CACAA	CTACC 11111 CTACC 11111 CTACC 11111 CTACC	TGGTC TGGTC 11111 TGGTC 11111 TGGTC	CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680	CGTCG CGTCG 11111 CGTCG 11111 CGTCG	ACGAC 11111 ACGAC 11111 ACGAC 690	ATCCC 11111 ATCCC 11111 ATCCC	CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700	TCGTG TCGTG 11111 TCGTG 11111 TCGTG	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 710	GGCTT 11111 GGCTT 11111 GGCTT	TCTTC 11111 TCTTC 11111 TCTTC 11111 TCTTC 720
¥22/1A B73/7-4 XI12/8A	CACAA 11111 CACAA 11111 CACAA	CTACC 11111 CTACC 11111 CTACC 11111 CTACC 670 CTCCT	TGGTC 11111 TGGTC 11111 TGGTC CTGGTC	CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680	CGTCG CGTCG 11111 CGTCG 11111 CGTCG GGGGC >	ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG	ATCCC 11111 ATCCC 11111 ATCCC CTTGT	CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA	TCGTG TCGTG 11111 TCGTG 11111 TCGTG TCCCC	CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA	GGCTT 11111 GGCTT 11111 GGCTT CATCC	TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG
W22/1A B73/7-4 X112/8A X112/8A	CACAA 11111 CACAA 11111 CACAA CTCGC	CTACC 11111 CTACC 11111 CTACC 11111 CTACC 670 CTCCT	TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT	CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 CGACC	CGTCG CGTCG 11111 CGTCG 11111 CGTCG  GGGGC  GGGGC  GGGGC	ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG	ATCCC 11111 ATCCC 11111 ATCCC CTTGT	CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA	TCGTG TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC	CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA	GGCTT 11111 GGCTT 11111 GGCTT CATCC CATCC	TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG
W22/1A B73/7-4 X112/8A X112/8A	CACAA 11111 CACAA 11111 CACAA CTCGC CTCGC 11111	CTACC 11111 CTACC 11111 CTACC 670 CTCCT CTCCT	TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT 11111	CTCGA CTCGA 11111 CTCGA 11111 CTCGA 680 CGACC	CGTCG 11111 CGTCG 11111 CGTCG CGTCG  GGGGC  GGGGC 1111	ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG CGGTG 11111	ATCCC 11111 ATCCC 11111 ATCCC CTTGT CTTGT 11111	CCGCG CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA CGACA 11111	TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC 11111	CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA AAGGA 11111	GGCTT 11111 GGCTT 11111 GGCTT CATCC CATCC 11111	TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG 11111
Y22/1A B73/7-4 X112/8A X112/8A Y22/1A	CACAA 11111 CACAA 11111 CACAA CTCGC 11111 CTCGC 11111	CTACC 11111 CTACC 11111 CTACC 670 CTCCT CTCCT 11111 CTCCT 11111	TGGTC 11111 TGGTC 11111 TGGTC CTGGT CTGGT 11111 CTGGT 11111	CTCGA CTCGA 11111 CTCGA 11111 CTCGA CGACC 11111 CGACC	CGTCG 11111 CGTCG 11111 CGTCG 11111 CGTCG  GGGGC  GGGGC 11111 aGGGC 11111	ACGAC 11111 ACGAC 11111 ACGAC 690 CGGTG 11111 CGGTG 11111	ATCCC 11111 ATCCC 11111 ATCCC CTTGT CTTGT 11111 CTTGT 11111	CCGCG 11111 CCGCG 11111 CCGCG 700 CGACA CGACA 11111 CGACA 11111	TCGTG 11111 TCGTG 11111 TCGTG TCCCC TCCCC 111111 TCCCC 111111	CAGGA 11111 CAGGA 11111 CAGGA 710 AAGGA AAGGA AAGGA 11111 AAGGA 11111	GGCTT 11111 GGCTT 11111 GGCTT CATCC CATCC 11111 CATCC 11111	TCTTC 11111 TCTTC 11111 TCTTC 720 AGCAG AGCAG 11111 AGCAG 11111

XI12/8A	CACAT	730	TCCCT	740 GTCTG			ATCAC			770 TACAT	TCCCC	780
YIIC/88	LAUAT	uucuu	TULLE	טונוט	UUHLA	MULLL	HIUHU	ונוטנ	CIGOG	INCHI	rucuc	uccii
A55\19	CAGAT	GGCGG	TGCCT	GTCTG	GGACA	AGCCC	ATGAG	TCTGC	CTGGG	TACAT	TGCGC	GCCTT
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4				GTCTG								
				11111								
XI12/8A	CAGAT	GGCGG	TGCCT	GTCTG	GGACA	AGCCC	ATGAG	TCTGC	CTGGG	TACAT	TGCGC	GCCTT
		700		000		910		020		020		040
VI 10/01	00044	790	הדרפר	800			CACCT		CTCTT	830	TCAAT	840
XI12/8A	LLLAA	はしししし	Clucu	ACTGA	טווטנ	TTUAU	CAUUT	ULIUL	ווטוט	טטווט	TUAAT	>
X22/1A	AATTT	GCCCC	GTGCG	ACTGA	GTTGC	TTGAG	CAGGT	GCTGC	GTCTT	67766	TGAAT	•
ALL/ III				11111								
B73/7-4				ACTGA								
				11111								
XI12/8A	CCCAA	GCCCC	CTGCG	ACTGA	GTTGC	TTGAG	CAGGT	GCTGC	GTCTT	GTTGG	TGAAT	CCCGG
		850					==.==			890	55510	900
X112/8A	CGCCC			860 GTTGG							GCGAC	
		TGTTC	TTTAT	GTTGG >	CGGTG	CGTGC	GCAGC	ATCTG	GTGAG	GAGTT		GCTTT
A8\S11X	CGCCC	TGTTC TGTTC	TTTAT TTTAT	GTTGG > GTTGG	CGGTG CGGTG	CGTGC GCTGC	GCAGC GCAGC	ATCTG ATCTG	GTGAG GTGAG	GAGTT GAGTT	GCGAC	GCTTT GCTTT
H22/1A	CGCCC 11111	TGTTC TGTTC 11111	TTTAT TTTAT 11111	GTTGG  STTGG  11 11	CGGTG CGGTG 11111	CGTGC GCTGC 11111	GCAGC GCAGC 11111	ATCTG ATCTG 11111	GTGAG GTGAG 11111	GAGTT GAGTT 11111	GCGAC 11111	GCTTT GCTTT 11111
	CGCCC 11111 CGCCC	TGTTC TGTTC 11111 TGTTC	TTTAT TTTAT 11111 TTTAT	GTTGG > GTTGG 11 11 GTgGG	CGGTG CGGTG 11111 CGGTG	CGTGC GCTGC 11111 GCTGC	GCAGC 11111 GCAGC	ATCTG ATCTG 11111 ATCTG	GTGAG GTGAG 11111 GTGAG	GAGTT GAGTT 11111 GAGTT	GCGAC 11111 GCGAC	GCTTT GCTTT 11111 GCTTT
W22/LA B73/7-4	CGCCC 11111 CGCCC 11111	TGTTC TGTTC 11111 TGTTC 11111	TTTAT TTTAT 11111 TTTAT 11111	GTTGG > GTTGG 11 11 GTgGG 11 11	CGGTG 11111 CGGTG 11111	CGTGC GCTGC 11111 GCTGC 11111	GCAGC 11111 GCAGC 11111	ATCTG 11111 ATCTG 11111	GTGAG GTGAG 11111 GTGAG 11111	GAGTT GAGTT 11111 GAGTT 11111	GCGAC 11111 GCGAC 11111	GCTTT 11111 GCTTT 11111
H22/1A	CGCCC 11111 CGCCC 11111	TGTTC TGTTC 11111 TGTTC 11111	TTTAT TTTAT 11111 TTTAT 11111	GTTGG > GTTGG 11 11 GTgGG	CGGTG 11111 CGGTG 11111	CGTGC GCTGC 11111 GCTGC 11111	GCAGC 11111 GCAGC 11111	ATCTG 11111 ATCTG 11111	GTGAG GTGAG 11111 GTGAG 11111	GAGTT GAGTT 11111 GAGTT 11111	GCGAC 11111 GCGAC 11111	GCTTT 11111 GCTTT 11111
W22/LA B73/7-4	CGCCC 11111 CGCCC 11111	TGTTC TGTTC 11111 TGTTC 11111	TTTAT TTTAT 11111 TTTAT 11111	GTTGG > GTTGG 11 11 GTgGG 11 11	CGGTG CGGTG 11111 CGGTG 11111 CGGTG	CGTGC GCTGC 11111 GCTGC 11111	GCAGC 11111 GCAGC 11111 GCAGC	ATCTG 11111 ATCTG 11111	GTGAG GTGAG 11111 GTGAG 11111 GTGAG	GAGTT GAGTT 11111 GAGTT 11111	GCGAC 11111 GCGAC 11111	GCTTT 11111 GCTTT 11111
W22/LA B73/7-4	CGCCC 11111 CGCCC 11111 CGCCC	TGTTC 11111 1GTTC 11111 1GTTC 11111 1GTTC	TTTAT TTTAT 11111 TTTAT 11111 TTTAT	GTTGG  STTGG  11 11  GTGGG  11 11  GTTGG	CGGTG 11111 CGGTG 11111 CGGTG	CGTGC GCTGC 11111 GCTGC 11111 GCTGC 930	GCAGC 11111 GCAGC 11111 GCAGC	ATCTG 11111 ATCTG 11111 ATCTG 940	GTGAG GTGAG 11111 GTGAG 11111 GTGAG	GAGTT 11111 GAGTT 11111 GAGTT 11111 GAGTT 950	GCGAC 11111 GCGAC 11111 GCGAC	GCTTT 11111 GCTTT 11111 GCTTT 960
U22/1A B73/7-4 XI12/8A	CGCCC 11111 CGCCC 11111 CGCCC	TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA	TTTAT TTTAT 11111 TTTAT 11111 TTTAT CTGGA	GTTGG  CTTGG  11 11  GTgGG  11 11  GTTGG  920  ATCCC	CGGTG CGGTG 11111 CGGTG 11111 CGGTG GGTCA	CGTGC GCTGC 11111 GCTGC 11111 GCTGC 930 CAACT	GCAGC 11111 GCAGC 11111 GCAGC ACTCT	ATCTG 11111 ATCTG 11111 ATCTG 4TCTG 940 TATGG	GTGAG GTGAG 11111 GTGAG 11111 GTGAG GCCTC	GAGTT 11111 GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA	GCGAC 11111 GCGAC 11111 GCGAC	GCTTT 11111 GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC
U22/1A B73/7-4 XI12/8A	CGCCC 11111 CGCCC 11111 CGCCC	TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA	TITAT TITAT HIHI TITAT HIHI TITAT CTGGA CTGGA	GTTGG  CTTGG  11 11  GTgGG  11 11  GTTGG  920  ATCCC	CGGTG 11111 CGGTG 11111 CGGTG GGTCA	CGTGC GCTGC 11111 GCTGC 11111 GCTGC 930 CAACT	GCAGC 11111 GCAGC 11111 GCAGC ACTCT	ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG	GTGAG GTGAG 11111 GTGAG 11111 GTGAG GCCTC	GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA	GCGAC 11111 GCGAC 11111 GCGAC CTTCC	GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC
W22/LA B73/7-4 XI12/8A XI12/8A	CGCCC 11111 CGCCC 11111 CGCCC GTGGA GTGGA 11111	TGTTC 11111 TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA 11111	TTTAT TTTAT 11111 TTTAT 11111 TTTAT CTGGA CTGGA 11111	GTTGG  CTTGG  11 11  GTgGG  11 11  GTTGG  920  ATCCC  ATCCC  11111	CGGTG 11111 CGGTG 11111 CGGTG GGTCA GGTCA 11111	CGTGC 11111 GCTGC 11111 GCTGC 930 CAACT CAACT 11111	GCAGC 11111 GCAGC 11111 GCAGC ACTCT ACTCT 11111	ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG 11111	GTGAG GTGAG 11111 GTGAG 11111 GTGAG GCCTC GCCTC 11111	GAGTT 11111 GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA GGCAA 11111	GCGAC 11111 GCGAC 11111 GCGAC CTTCC 11111	GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC CCAGC 11111
W22/LA B73/7-4 XI12/8A XI12/8A	CGCCC 11111 CGCCC 11111 CGCCC GTGGA GTGGA 11111 GTGGA	TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA 11111 GCTGA	TITAT TITAT HIHI TITAT HIHI TITAT CTGGA CTGGA HIHI CTGGA	GTTGG  CTTGG  11 11  GTgGG  11 11  GTTGG  920  ATCCC  ATCCC  11111  ATCCC	CGGTG 11111 CGGTG 11111 CGGTG GGTCA 11111 GGTCA	CGTGC 11111 GCTGC 11111 GCTGC 930 CAACT 11111 CAACT	GCAGC 11111 GCAGC 11111 GCAGC ACTCT ACTCT 11111 ACTCT	ATCTG 11111 ATCTG 11111 ATCTG 940 TATGG 11111 TATGG	GTGAG 11111 GTGAG 11111 GTGAG GCCTC GCCTC 11111 GCCTC	GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA 11111 GGCAA	GCGAC 11111 GCGAC 11111 GCGAC CTTCC 11111 CTTCC	GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC 11111 CCAGC
W22/1A B73/7-4 X112/8A X112/8A W22/1A	CGCCC 11111 CGCCC 11111 CGCCC GTGGA GTGGA 11111 GTGGA 11111	TGTTC 11111 TGTTC 11111 TGTTC 910 GCTGA 11111 GCTGA 11111	TTTAT TTTAT 11111 TTTAT 11111 TTTAT CTGGA CTGGA 11111 CTGGA 11111	GTTGG  CTTGG  11 11  GTgGG  11 11  GTTGG  920  ATCCC  ATCCC  11111	CGGTG 11111 CGGTG 11111 CGGTG GGTCA GGTCA 11111 GGTCA 11111	CGTGC 11111 GCTGC 11111 GCTGC 930 CAACT CAACT 11111 CAACT 11111	GCAGC 11111 GCAGC 11111 GCAGC ACTCT ACTCT 11111 ACTCT 11111	ATCTG 11111 ATCTG 11111 ATCTG 740 TATGG 11111 TATGG 11111	GTGAG  GTGAG  11111  GTGAG  11111  GTGAG  GCCTC  GCCTC  11111  GCCTC  11111	GAGTT 11111 GAGTT 11111 GAGTT 11111 GAGTT 950 GGCAA GGCAA 11111 GGCAA 11111	GCGAC 11111 GCGAC 11111 GCGAC CTTCC CTTCC 11111 CTTCC 11111	GCTTT 11111 GCTTT 11111 GCTTT 960 CCAGC CCAGC 11111 CCAGC 11111

		970		980		990		1000		1010		1020
XI12/8A	GACGA	CCCAC	TGTCT									
H22/1A			TGTCT									
			11111									
B73/7-4			TGTCT									
			11111									
A8/211X	GACGA	CCCAC	TGTCT	CTGCG	CATGC	TAGGT	ATGCA	TGGCA	CGGTG	TATGC	AAATT	ATGCA
		1030		1040		1050		1060		1070		1080
XI12/8A	GTGGA		CCGAT									
A55/1V												CAGGG>
			11111									
B73/7-4												CAGGG>
			11111									
XI12/8A	GTGGA	TAAGG	CCGAT	CTGTT	GCTTG	CACTT	GGTGT	GCGGT	TTGAT	GATCG	TGTGA	CAGGG
		1000		1100		1110		1120		1120	:	1140
VI12/QA	AAGAT		rtttt									
A8/S11X	AAGAT											
XI12/8A W22/1A		TGAGG		GCAAG	CAGGG	CTAAG	ATTGT	GCACG	TTGAT	ATTGA	TCCGG	CTGAG
	AAGAT	TGAGG TGAGG	CTTTT	GCAAG GCAAG	CAGGG CAGGG	CTAAG CTAAG	ATTGT ATTGT	GCACG GCACG	TTGAT TTGAT	ATTGA	TCCGG TCCGG	CTGAG CTGAG
	AAGAT	TGAGG TGAGG 11111	CTTTT	GCAAG 11111	CAGGG CAGGG 11111	CTAAG CTAAG 11111	ATTGT ATTGT 11111	GCACG GCACG 11111	TTGAT TTGAT 11111	ATTGA ATTGA 11111	TCCGG TCCGG 11111	CTGAG CTGAG 11111
W22/1A	AAGAT 11111 AAGAT	TGAGG TGAGG 11111 TGAGG	CTTTT CTTTT 11111	GCAAG 11111 GCAAG	CAGGG CAGGG 11111 CAGGG	CTAAG CTAAG 11111 CTAAG	ATTGT ATTGT 11111 ATTGT	GCACG GCACG 11111 GCACG	TTGAT TTGAT 11111 TTGAT	ATTGA ATTGA 11111 ATTGA	TCCGG 11111 TCCGG	CTGAG CTGAG 11111 CTGAG
W22/1A	AAGAT 11111 AAGAT 11111	TGAGG 11111 TGAGG 11111	CTTTT CTTTT 11111 CTTTT	GCAAG 11111 GCAAG 11111	CAGGG 11111 CAGGG 11111	CTAAG 11111 CTAAG 11111	ATTGT 11111 ATTGT 11111	GCACG 11111 GCACG 11111	TTGAT TTGAT 11111 TTGAT 11111	ATTGA ATTGA 11111 ATTGA 11111	TCCGG 11111 TCCGG 11111	CTGAG CTGAG 11111 CTGAG 11111
W22/1A B73/7-4	AAGAT 11111 AAGAT 11111	TGAGG TGAGG 11111 TGAGG 11111 TGAGG	CTTTT  CTTTT  11111  CTTTT  11111  CTTTT	GCAAG 11111 GCAAG 11111 GCAAG	CAGGG 11111 CAGGG 11111 CAGGG	CTAAG 11111 CTAAG 11111 CTAAG	ATTGT 11111 ATTGT 11111 ATTGT ATTGT	GCACG 11111 GCACG 11111 GCACG	TTGAT TTGAT 11111 TTGAT 11111 TTGAT	ATTGA 11111 ATTGA 11111 ATTGA	TCCGG 11111 TCCGG 11111 TCCGG	CTGAG 11111 CTGAG 11111 CTGAG
W22/1A B73/7-4 XI12/8A	AAGAT 11111 AAGAT 11111 AAGAT	TGAGG TGAGG 11111 TGAGG 11111 TGAGG 1150	CTTTT 11111 CTTTT 11111 CTTTT CTTTT	GCAAG 11111 GCAAG 11111 GCAAG 11111 GCAAG	CAGGG 11111 CAGGG 11111 CAGGG	CTAAG 11111 CTAAG 11111 CTAAG 1170	ATTGT 11111 ATTGT 11111 ATTGT ATTGT	GCACG GCACG 11111 GCACG 11111 GCACG 1180	TTGAT TTGAT 11111 TTGAT 11111 TTGAT	ATTGA 11111 ATTGA 11111 ATTGA 11111 ATTGA	TCCGG TCCGG 11111 TCCGG 11111 TCCGG	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200
W22/1A B73/7-4	AAGAT 11111 AAGAT 11111 AAGAT	TGAGG TGAGG 11111 TGAGG 11111 TGAGG 1150	CTTTT 11111 CTTTT 11111 CTTTT CTTTT	GCAAG 11111 GCAAG 11111 GCAAG 11111 GCAAG	CAGGG 11111 CAGGG 11111 CAGGG	CTAAG 11111 CTAAG 11111 CTAAG 1170	ATTGT 11111 ATTGT 11111 ATTGT ATTGT	GCACG GCACG 11111 GCACG 11111 GCACG 1180	TTGAT TTGAT 11111 TTGAT 11111 TTGAT	ATTGA 11111 ATTGA 11111 ATTGA 11111 ATTGA	TCCGG TCCGG 11111 TCCGG 11111 TCCGG	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200
W22/1A B73/7-4 XI12/8A	AAGAT 11111 AAGAT 11111 AAGAT	TGAGG TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA	CTTTT 11111 CTTTT 11111 CTTTT ACAAG	GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC	CAGGG 11111 CAGGG 11111 CAGGG ACATG	CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC	ATTGT 11111 ATTGT 11111 ATTGT ATTGT	GCACG 11111 GCACG 11111 GCACG 11180 TGCAG	TTGAT TTGAT 11111 TTGAT 11111 TTGAT ATGTT	ATTGA 11111 ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT	TCCGG TCCGG 11111 TCCGG 11111 TCCGG	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200  TGCAG
W22/1A B73/7-4 XI12/8A XI12/8A	AAGAT 11111 AAGAT 11111 AAGAT ATTGG	TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA	CTTTT 11111 CTTTT 11111 CTTTT CTTTT	GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC	CAGGG 11111 CAGGG 11111 CAGGG ACATG	CTAAG 11111 CTAAG 11111 CTAAG 11170 TGTCC TGTCC	ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG	GCACG 11111 GCACG 11111 GCACG 1180 TGCAG	TTGAT 11111 TTGAT 11111 TTGAT 11111 TTGAT ATGTT	ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT	TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200  TGCAG
W22/1A B73/7-4 XI12/8A XI12/8A	AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111	TGAGG TGAGG TITT TGAGG TTT TGAGG TTT TGAGG TTT TGAGG TTT TGAGG TTT TGAGA TTT TT TGAGA TT	CTTTT 11111 CTTTT 11111 CTTTT ACAAG ACAAG 11111	GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC CAGCC 11111	CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG	CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC TGTCC 11111	ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG 11111	GCACG 11111 GCACG 11111 GCACG 1180 TGCAG TGCAG 11111	TTGAT TTGAT 11111 TTGAT 11111 TTGAT ATGTT 11111	ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT AAGCT 11111	TCCGG 11111 TCCGG 11111 TCCGG TGCTT TGCTT 11111	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200  TGCAG  TGCAG  11111
W22/1A B73/7-4 X112/8A X112/8A W22/1A	AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111 ATTGG	TGAGG 11111 TGAGG 11111 TGAGG 1150 CAAGA CAAGA	CTTTT 11111 CTTTT 11111 CTTTT ACAAG	GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC CAGCC 11111 CAGCC	CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG 11111 ACATG	CTAAG 11111 CTAAG 11111 CTAAG 1170 TGTCC 11111 TGTCC	ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG 11111 ATCTG	GCACG 11111 GCACG 11111 GCACG 1180 TGCAG 11111 TGCAG	TTGAT 11111 TTGAT 11111 TTGAT ATGTT ATGTT 11111 ATGTT	ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT 11111 AAGCT	TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT 11111 TGCTT	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200  TGCAG  TGCAG  11111  TGCAG
W22/1A B73/7-4 X112/8A X112/8A W22/1A	AAGAT 11111 AAGAT 11111 AAGAT ATTGG 11111 ATTGG 11111	TGAGG TGAGG TITT TGAGG TTT TGAGG TTT TGAGG TTT TGAGG TTT TGAGA TTT TGAGAG TTT TTT	CTTTT 11111 CTTTT 11111 CTTTT ACAAG ACAAG 11111 ACAAG	GCAAG 11111 GCAAG 11111 GCAAG 1160 CAGCC CAGCC 11111 CAGCC 11111	CAGGG 11111 CAGGG 11111 CAGGG ACATG ACATG 11111 ACATG 11111	CTAAG 11111 CTAAG 11111 CTAAG 11170 TGTCC TGTCC 11111 TGTCC 11111	ATTGT 11111 ATTGT 11111 ATTGT ATCTG ATCTG 11111 ATCTG 11111	GCACG 11111 GCACG 11111 GCACG 1180 TGCAG TGCAG 11111 TGCAG 11111	TTGAT TTGAT 11111 TTGAT 11111 TTGAT ATGTT ATGTT 11111 ATGTT 11111	ATTGA 11111 ATTGA 11111 ATTGA 1190 AAGCT AAGCT 11111 AAGCT 11111	TCCGG 11111 TCCGG 11111 TCCGG 11111 TCCGG TGCTT TGCTT 11111 TGCTT 11111	CTGAG  CTGAG  11111  CTGAG  11111  CTGAG  1200  TGCAG  TGCAG  11111  TGCAG  11111

		1210		1220		1230		1240		1250		1260
XI12/8A	GGCAT	GAATG	CTCTT	CTTGA	AGGAA	GCACA	TCAAA	GAAGA	GCTTT	GACTT	TGGCT	CATGG
W22/1A	GGCAT	GAATG	CTCTT	CTTGA	AGGAA	GCACA	TCAAA	GAAGA	GCTTT	GACTT	TGGCT	CATGG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4	GGCAT	GAATG	CTCTT	CTTGA	AGGAA	GCACA	TCAAA	GAAGA	GCTTT	GACTT	TGGCT	CATGG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
XI12/8A	GGCAT	GAATG	CTCTT	CTTGA	AGGAA	GCACA	TCAAA	GAAGA	GCTTT	GACTT	TGGCT	CATGG
		1270		1200		1200		1200		1210		1220
V112/0A	AACCA	1270	TCCAT	1280	CAACA				CCTAT	1310	ATCTA	1320
X112/8A	AACUA	IUAUI	TUUNT	CHUCH	UMMUM	uuunn	11666	CCIIU	ואוטט	AAAAC	AICIA	טאטוא
H22/1A	AACGA	TGAGT	TGGAT	CAGCA	GAAGA	GGGAA	TTCCC	CCTTG	GGTAT	AAAAC	ATCTA	ATGAG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/65	AACGA	TGAGT	TGGAT	CAGCA	GAAGA	GGGAA	TTCCC	CCTTG	<b>GGTAT</b>	AAAAC	<b>ATCTA</b>	ATGAG
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
XI12/8A	AACGA	TGAGT	TGGAT	CAGCA	GAAGA	GGGAA	TTCCC	CCTTG	GGTAT	AAAAC	ATCTA	ATGAG
		1220		1240		1250		1240		1270		1201
40/C11V	CACAT	1330	AAAA	1340 TATEC	TATTO		rttc.		TCACC	1370	רבאבב	1380
X112/8A	GAGAT		CACAA		TATTC				TGACG	1370 AAAGG	CGAGG	
XI12/8A U22/1A		CCAGC		TATGC		AGGTT	CTTGA	TGAGC				CCATC
	GAGAT	CCAGC CCAGC	CACAA	TATGC TATGC	TATTC	AGGTT AGGTT	CTTGA CTTGA	TGAGC TGAGC	TGACG	AAAGG	CGAGG	CCATC CCATC
	GAGAT 11111 GAGAT	CCAGC CCAGC 11111 CCAGC	CACAA 11111 CACAA	TATGC TATGC 11111 TATGC	TATTC 11111 TATTC	AGGTT AGGTT 11111 AGGTT	CTTGA CTTGA 11111 CTTGA	TGAGC TGAGC 11111 TGAGC	TGACG 11111 TGACG	AAAGG 11111 AAAGG	CGAGG 11111 CGAGG	CCATC CCATC 11111 CCATC
W22/1A	GAGAT 11111 GAGAT 11111	CCAGC 11111 CCAGC 11111	CACAA 11111 CACAA 11111	TATGC TATGC 11111 TATGC 11111	TATTC 11111 TATTC 11111	AGGTT 11111 AGGTT 11111	CTTGA CTTGA 11111 CTTGA 11111	TGAGC 11111 TGAGC 11111	TGACG 11111 TGACG 11111	AAAGG 11111 AAAGG 11111	CGAGG 11111 CGAGG 11111	CCATC 11111 CCATC 11111
W22/1A	GAGAT 11111 GAGAT 11111	CCAGC 11111 CCAGC 11111	CACAA 11111 CACAA 11111	TATGC TATGC 11111 TATGC 11111	TATTC 11111 TATTC 11111	AGGTT 11111 AGGTT 11111	CTTGA CTTGA 11111 CTTGA 11111	TGAGC 11111 TGAGC 11111	TGACG 11111 TGACG 11111	AAAGG 11111 AAAGG	CGAGG 11111 CGAGG 11111	CCATC 11111 CCATC 11111
H22/1A B73/7-4	GAGAT 11111 GAGAT 11111	CCAGC CCAGC 11111 CCAGC 11111 CCAGC	CACAA 11111 CACAA 11111	TATGC TATGC 11111 TATGC 11111 TATGC	TATTC 11111 TATTC 11111	AGGTT 11111 AGGTT 11111 AGGTT AGGTT	CTTGA CTTGA 11111 CTTGA 11111 CTTGA	TGAGC TGAGC 11111 TGAGC 11111 TGAGC	TGACG 11111 TGACG 11111	AAAGG 11111 AAAGG 11111 AAAGG	CGAGG 11111 CGAGG 11111	CCATC CCATC 11111 CCATC 11111 CCATC
H22/1A B73/7-4 XI12/8A	GAGAT 11111 GAGAT 11111 GAGAT	CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC	CACAA 11111 CACAA 11111 CACAA	TATGC TATGC 11111 TATGC 11111 TATGC 1400	TATTC 11111 TATTC 11111 TATTC	AGGTT 11111 AGGTT 11111 AGGTT 1410	CTTGA CTTGA 11111 CTTGA 11111 CTTGA	TGAGC TGAGC 11111 TGAGC 11111 TGAGC	TGACG 11111 TGACG 11111 TGACG	AAAGG 11111 AAAGG 11111 AAAGG 1430	CGAGG 11111 CGAGG 11111 CGAGG	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440
H22/1A B73/7-4	GAGAT 11111 GAGAT 11111 GAGAT	CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC	CACAA 11111 CACAA 11111 CACAA	TATGC TATGC 11111 TATGC 11111 TATGC 1400	TATTC 11111 TATTC 11111 TATTC	AGGTT 11111 AGGTT 11111 AGGTT 1410	CTTGA CTTGA 11111 CTTGA 11111 CTTGA	TGAGC TGAGC 11111 TGAGC 11111 TGAGC	TGACG 11111 TGACG 11111 TGACG	AAAGG 11111 AAAGG 11111 AAAGG	CGAGG 11111 CGAGG 11111 CGAGG	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440
H22/1A B73/7-4 XI12/8A	GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG	CCAGC CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG	CACAA 11111 CACAA 11111 CACAA GTGTT	TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA	TATTC 11111 TATTC 11111 TATTC GCACC	AGGTT 11111 AGGTT 11111 AGGTT 11111 AGGTT AGATG AGATG	CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC	TGAGC TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC	TGACG 11111 TGACG 11111 TGACG AGTAC	AAAGG 11111 AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC	CGAGG 11111 CGAGG 11111 CGAGG TTACA	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 AGCGG AGCGG
H22/1A B73/7-4 XI12/8A XI12/8A	GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111	CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111	CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111	TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111	TATTC 11111 TATTC 11111 TATTC GCACC GCACC	AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111	CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111	TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC GGCAC 11111	TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC	AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC TACAC 11111	CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 AGCGG 11111
H22/1A B73/7-4 XI12/8A XI12/8A	GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111 ATCGG	CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 CACAG	CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 GTGTT	TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 GGGCA	TATTC 11111 TATTC 11111 TATTC GCACC GCACC 11111 GCACC	AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 AGATG	CTTGA CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111 TGGGC	TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC GGCAC 11111 GGCAC	TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 AGTAC	AAAGG 11111 AAAGG 11111 AAAGG 11111 AAAAGG TACAC TACAC 11111 TACAC	CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA 11111 TTACA	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 AGCGG 11111 AGCGG
H22/1A B73/7-4 XI12/8A XI12/8A H22/1A	GAGAT 11111 GAGAT 11111 GAGAT ATCGG ATCGG 11111 ATCGG 11111	CCAGC 11111 CCAGC 11111 CCAGC 11111 CCAGC 1390 CACAG CACAG 11111 CACAG 11111	CACAA 11111 CACAA 11111 CACAA GTGTT GTGTT 11111 GTGTT 11111	TATGC TATGC 11111 TATGC 11111 TATGC 1400 GGGCA GGGCA 11111 GGGCA 11111	TATTC 11111 TATTC 11111 TATTC GCACC I1111 GCACC 11111	AGGTT 11111 AGGTT 11111 AGGTT 1410 AGATG 11111 AGATG 11111	CTTGA 11111 CTTGA 11111 CTTGA 11111 CTTGA TGGGC TGGGC 11111 TGGGC 11111	TGAGC 11111 TGAGC 11111 TGAGC 1420 GGCAC GGCAC 11111 GGCAC 11111	TGACG 11111 TGACG 11111 TGACG AGTAC AGTAC 11111 AGTAC 11111	AAAGG 11111 AAAGG 11111 AAAGG 1430 TACAC TACAC 11111	CGAGG 11111 CGAGG 11111 CGAGG TTACA TTACA 11111 TTACA 11111	CCATC 11111 CCATC 11111 CCATC 11111 CCATC 1440 AGCGG 11111 AGCGG 11111

		1450				1470		1480		1490		1500
X112/8A	CCAAG (	GCAGT	GGTTG	TCTTC	AGCTG	GTCTT	GGGGC	TATGG	GATTT	GGTTT	GCCGG	CTGCT
A55\IV	CCAAG (											
	11111											
B73/7-4	CCAAG (											
	11111 1											
X112/8A	CCAAG (	GCAGT	GGTTG	TCTTC	AGCTG	GTCTT	GGGGC	TATGG	GATTT	GGTTT	GCCGG	CTGCT
		1510	,	1520		1530		1540		1550		1560
XI12/8A	GCTGG	TGCTT	CTGTG	GCCAA	CCCAG	GTGTT	ACTGT	TGTTG	ACATC	GATGG	AGATG	GTAGC
						>						
A55\1V	GCTGG											
	11111						•					
B73/7-4	GCTGG T											
	11111											_
XI12/8A	GCTGG	TGCTT	CTGTG	GCCAA	CCCAG	GTGTT	ACTGT	TGTTG	ACATC	GATGG	AGATG	GTAGC
		4534				4500		1700		1215		1600
	TTTOT	1570	40CTT	1580			A 7.00.5				CCTCA	1620
A8/S11X	TITCT		ACGTT								GGTGA	
	TITCT (	CATGA		CAGGA	GCTAG	CTATG	ATCCG	AATTG	AGAAC	CTCCC	<b>&gt;</b>	AGGTC
XI12/8A U22/1A		CATGA Catga	ACGTT	CAGGA CAGGA	GCTAG GCTAG	CTATG CTATG	ATCCG ATCCG	AATTG AATTG	AGAAC AGAAC	CTCCC	> GGTGA	AGGTC
	TTTCT	CATGA Catga 11111	ACGTT	CAGGA CAGGA 11111	GCTAG GCTAG 11111	CTATG CTATG 11111	ATCCG ATCCG 11111	AATTG 11111	AGAAC 11111	CTCCC CTCCC 11111	> GGTGA 1111	AGGTC AGGTC 11111
H22/1A	TTTCT (	CATGA CATGA 11111 CATGA	ACGTT 11111 ACGTT	CAGGA CAGGA 11111 CAGGA	GCTAG GCTAG 11111 GCTAG	CTATG CTATG 11111 CTATG	ATCCG 11111 ATCCG	AATTG 11111 AATTG	AGAAC 11111 AGAAC	CTCCC 11111 CTCCC	GGTGA 1111 aGTGA	AGGTC AGGTC 11111
H22/1A	TTTCT (	CATGA CATGA 11111 CATGA 11111	ACGTT 11111 ACGTT 11111	CAGGA CAGGA 11111 CAGGA 11111	GCTAG 11111 GCTAG 11111	CTATG 11111 CTATG 11111	ATCCG 11111 ATCCG 11111	AATTG 11111 AATTG 11111	AGAAC 11111 AGAAC 11111	CTCCC 11111 CTCCC 11111	GGTGA 1111 aGTGA 1111	AGGTC 11111 AGGTC 11111
H22/1A B73/7-4	TTTCT ( 11111 TTTCT ( 11111	CATGA CATGA 11111 CATGA 11111 CATGA	ACGTT 11111 ACGTT 11111	CAGGA CAGGA 11111 CAGGA 11111 CAGGA	GCTAG GCTAG 11111 GCTAG 11111 GCTAG	CTATG CTATG 11111 CTATG 11111 CTATG	ATCCG 11111 ATCCG 11111 ATCCG	AATTG 11111 AATTG 11111 AATTG	AGAAC 11111 AGAAC 11111 AGAAC	CTCCC CTCCC IIIII CTCCC IIIII CTCCC	GGTGA 1111 aGTGA 1111	AGGTC 11111 AGGTC 11111 AGGTC
W22/1A B73/7-4 XI12/8A	TTTCT ( 11111 TTTCT ( 11111 TTTCT (	CATGA 11111 CATGA 11111 CATGA 11111 CATGA	ACGTT 11111 ACGTT 11111 ACGTT	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640	GCTAG GCTAG 11111 GCTAG 11111 GCTAG	CTATG 11111 CTATG 11111 CTATG 11111 CTATG 1650	ATCCG 11111 ATCCG 11111 ATCCG	AATTG 11111 AATTG 11111 AATTG 11111 AATTG	AGAAC 11111 AGAAC 11111 AGAAC	CTCCC 11111 CTCCC 11111 CTCCC 1670	SGTGA 1111 QGTGA 1111 GGTGA	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680
H22/1A B73/7-4	TTTCT ( 11111 TTTCT ( 11111	CATGA 11111 CATGA 11111 CATGA 11111 CATGA	ACGTT 11111 ACGTT 11111 ACGTT	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640	GCTAG GCTAG 11111 GCTAG 11111 GCTAG	CTATG 11111 CTATG 11111 CTATG 11111 CTATG 1650	ATCCG 11111 ATCCG 11111 ATCCG	AATTG 11111 AATTG 11111 AATTG 11111 AATTG	AGAAC 11111 AGAAC 11111 AGAAC	CTCCC 11111 CTCCC 11111 CTCCC 1670	SGTGA 1111 QGTGA 1111 GGTGA	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680
W22/1A B73/7-4 XI12/8A	TTTCT ( 11111 TTTCT ( 11111 TTTCT ( TT	CATGA CATGA 11111 CATGA 11111 CATGA 1630 GCTAA	ACGTT 11111 ACGTT 11111 ACGTT ACAAC	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 1640 CAGCA	GCTAG 11111 GCTAG 11111 GCTAG CCTGG	CTATG 11111 CTATG 11111 CTATG 1650 GGATG	ATCCG 11111 ATCCG 11111 ATCCG GTGGT	AATTG 11111 AATTG 11111 AATTG 1660 GCAGT	AGAAC 11111 AGAAC 11111 AGAAC GGGAG	CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG	GGTGA 1111 0GTGA 1111 GGTGA GTTCT	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG
W22/1A B73/7-4 X112/8A X112/8A	TTTCT ( 11111	CATGA 11111 CATGA 11111 CATGA 1630 GCTAA 11111	ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC 11111	CAGGA CAGGA 11111 CAGGA 11111 CAGGA 11111 CAGGA CAGCA CAGCA	GCTAG 11111 GCTAG 11111 GCTAG CCTGG CCTGG 11111	CTATG 11111 CTATG 11111 CTATG 1650 GGATG 11111	ATCCG 11111 ATCCG 11111 ATCCG GTGGT GTGGT 11111	AATTG 11111 AATTG 11111 AATTG 1660 GCAGT GCAGT 11111	AGAAC 11111 AGAAC 11111 AGAAC GGGAG GGGAG 11111	CTCCC CTCCC IIIII CTCCC IIIII CTCCC I670 GACAG GACAG IIIII	GGTGA 1111 GGTGA 1111 GGTGA GTTCT GTTCT 11111	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111
W22/1A B73/7-4 X112/8A X112/8A	TTTCT ( 11111	CATGA CATGA 11111 CATGA 11111 CATGA GCTAA 11111 GCTAA	ACGTT 11111 ACGTT 11111 ACGTT ACAAC ACAAC 11111 ACAAC	CAGGA CAGGA 11111 CAGGA 11111 CAGGA CAGCA CAGCA 11111 CAGCA	GCTAG 11111 GCTAG 11111 GCTAG CCTGG 11111 CCTGG	CTATG 11111 CTATG 11111 CTATG 1650 GGATG GGATG 11111 GGATG	ATCCG 11111 ATCCG 11111 ATCCG GTGGT 11111 GTGGT	AATTG 11111 AATTG 11111 AATTG 1660 GCAGT 11111 GCAGT	AGAAC 11111 AGAAC 11111 AGAAC GGGAG 11111 GGGAG	CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG 11111 GACAG	GGTGA 1111 0GTGA 1111 GGTGA GTTCT 11111 GTTCT	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111 ATAAG
W22/1A B73/7-4 X112/8A X112/8A W22/1A	TTTCT ( 11111	CATGA 11111 CATGA 11111 CATGA 1630 GCTAA 11111 GCTAA 11111	ACGTT 11111 ACGTT 11111 ACGAC ACAAC 11111 ACAAC 11111	CAGGA CAGGA 11111 CAGGA 11111 CAGGA CAGCA CAGCA 11111 CAGCA 11111	GCTAG 11111 GCTAG 11111 GCTAG CCTGG CCTGG 11111 CCTGG 11111	CTATG 11111 CTATG 11111 CTATG 1650 GGATG 11111 GGATG 11111	ATCCG 11111 ATCCG 11111 ATCCG GTGGT GTGGT 11111	AATTG 11111 AATTG 11111 AATTG 1660 GCAGT 11111 GCAGT 11111	AGAAC 11111 AGAAC 11111 AGAAC GGGAG GGGAG 11111 GGGAG 11111	CTCCC 11111 CTCCC 11111 CTCCC 1670 GACAG 11111 GACAG 11111	GGTGA 1111 GGTGA 1111 GGTGA GTTCT GTTCT 11111 GTTCT 11111	AGGTC 11111 AGGTC 11111 AGGTC 11111 AGGTC 1680 ATAAG ATAAG 11111 ATAAG 11111

		1690		1700		1710		1720		1730		1740
XI12/8A	GCCAA	CAGAG	CGCAC	ACATA	CTTGG	GAAAC	CCAGA	GAATG	AAAGT	GAGAT	ATATC	CAGAT
455\IV								GAATG				
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4	GCCAA	CAGAG	CGCAC	<b>ACATA</b>	CTTGG	GAAAC	CCAGA	GAATG	AAAGT	GAGAT	<b>ATATC</b>	CAGAT
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
XI12/8A	GCCAA	CAGAG	CGCAC	ACATA	CTTGG	GAAAC	CCAGA	GAATG	AAAGT	GAGAT	ATATC	CAGAT
		1750		1760		1770		1780		1790		1800
XI12/8A	TTCGT	GACGA	TCGCC	AAAGG	GTTCA	ACATT	CCAGC	GGTCC	GTGTG	ACAAA	GAAGA	ACGAA
H22/1A	TTCGT	GACGA	TCGCC	AAAGG	GTTCA	ACATT	CCAGC	GGTCC	GTGTG	ACAAA	GAAGA	ACGAA
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4	TTCGT	GACGA	TCGCC	AAAGG	GTTCA	ACATT	CCAGC	GGTCC	GTGTG	ACAAA	GAAGA	ACGAA
,								11111				
X112/8A								GGTCC				
		1810		1820		1830		1840		1850		1860
XI12/8A	GTCCG	CGCAG	CGATA	AAGAA	GATGC	TCGAG	ACTCC	AGGGC	CGTAC	CTCTT	GGATA	TAATC
H22/1A	GTCCG	CGCAG	CGATA	AAGAA	GATGC	TCGAG	ACTCC	AGGGC	CGTAC	СТСТТ	GGATA	TAATC
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
B73/7-4	GTCCG	CGCAG	CGATA	AAGAA	GATGC	TCGAG	ACTCC	AGGGC	CGTAC	CTCTT	GGATA	TAATC
	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111	11111
XI12/8A								AGGGC				
		1870		1880		1890		1900		1910		1920
XI12/8A	GTCCC							TAATG				
422/1A	GTCCC	ACACC	AGGAG	CATGT	GTTGC	CTATG	ATCCC	TAgTG	GTGGG	GCTTT	CAAGG	ATATG
•								11111				
B73/7-4								TAgTG				
								11 11				
XI12/8A								TAATG				

		1930		1940		1950		1960		
XI12/8A	ATCCT	GGATG	GTGAT	GGCAG	GACTG	TGTAC	TGATC	TAAAA	TCCAG	CAAG
A1/25A	ATCCT	GGATG	GTGAT	GGCAG	GACTG	TGTAC	TGATC	ΤΑΑΑΑ	TCCAG	CAAGS
**************************************	11111									
B73/7-4	ATCCT	GGATG	GTGAT	GGCAG	GACTG	TGTAC	TGATC	TAAAA	TCCAG	CAAG>
	11111	11111	11111	11111	11111	11111	11111	11111	11111	1111
XI12/8A	ATCCT	GGATG	GTGAT	GGCAG	GACTG	TGTAC	TGATC	TAAAA	TCCAG	CAAG

FIG.7 I

	11	0 2	0	30	40	50	60
XI12/8A	MATAA AASTA	LTGAT TAAPK	ARRRA HLLA	T RRALA APIR	C SAASP	AMPHA PPATP	LRPYG
A55/19	* * *	LTGAT TAAPK					
B73/7-4	MATAA AASTA	LTGAT TAAPK	ARRRA HLLA	T RRALA APIR	C SAASP	AMPHA PPATP	LRPYG
XI12/8A		11111 11111 LTGAT TAAPK					
	-			00	00	140	
XI12/8A	DTNDD KCANI	U 8 LVESL ERCGV	O DIVEN YDGG				0S1
V11C/ 0H	וואט אותו ו K עמטאד	LACOT FUCUA	אטעא וו טט	n Shlii whli	N 3) VIN	MILIK HEGOL	nı nnə
H22/1A		LYESL ERCGY					
B== 15 1		11111 11111					
B73/7-4		LVESL ERCGV					
XI12/8A		LAE2T EBCCA					
	13	n 14	0 1	50 1	.60	170	180
X112/8A	<del>-</del> -	G VCIAT SGPG	-				
M55\1V		G VCIAT SGPG					
n-20 <i>1</i> 2 4		1 11111 1111 1					
B73/7-4		G YCIAT SGPG 1 11111 1111				•	
XI12/8A		G VCIAT SGPG					
	19	0 20	nn 2	10 8	)2R	230	240
A8/211X		N YLVLD YDDI	-				
#55\I\		N YLVLD VDDI					
D79/7 /		1 11111 1111 N. V. V. D. V.D.					
B73/7-4		IN YLVLD VDDI 1 11111 1111					
XI12/8A		N AFAFD ADDI					

XI12/8A	LPGYI	250 Arlpk	PPATE	LLEQV	LRLVG	270 ESRRP	VLYVG	280 GGCAA	SGEEL	290 RRFVE	LTGIP	300 VTTTL
H55/19								GGCAA 11111				
B73/7-4								GGCAA 11111				
XI12/8A								GGCAA				
		310		320		330		340		350		360
XI12/8A	HGLGN	FPSDD	PLSLR	MLGMH	GTVYA	NYAVD	KADLL	LALGV	RFDDR	ALCKI	EAFAS	RAK 1 V
W22/1A								LALGV				
B73/7-4			11111 PLSLR					LALGY	11111 RFDDR		11111 EAFAS	
XI12/8A								11111 LALGV				
// LIL/ UII	1106411			1142 657 117			*****			* 1 6314	214110	******
		070		004		000		400		44.0		400
XI12/8A	HVDID	370 PAEIG	KNKQP	380 382	ADVKL	390 Alqgh	NALLE	400 GSTSK	KSFDF	410 GSYND	ELDQQ	420 Krefp
X112/8A #22/1A	HVDID	PAEIG PAEIG	KNKQP	HA21C	ADVKL	ALQGM ALQGM	NALLE	C212K	KSFDF	CZAND CZAND	ELDQQ	KREFP KREFP
	HVDID 11111 HVDID	PAEIG PAEIG 11111 PAEIG	KNKQP 11111 KNKQP	HVSIC 11111 HVSIC	ADVKL 11111 ADVKL	ALQGM ALQGM 11111 ALQGM	NALLE 11111 NALLE	G212K 11111 G212K	KSFDF 11111 KSFDF	CSAND 11111 CSAND CSAND	ELDQQ 11111 ELDQQ	KREFP KREFP 11111 KREFP
H22/1A	HVDID 11111 HVDID 11111	PAEIG 11111 PAEIG 11111	KNKQP 11111 KNKQP	HVSIC 11111 HVSIC 11111	ADVKL 11111 ADVKL	ALQGM 11111 ALQGM 11111	NALLE 11111 NALLE 11111	G212K	KSFDF 11111 KSFDF 11111	11111 62AND 11111 62AND	ELDQQ 11111 ELDQQ 11111	KREFP KREFP 11111 KREFP 11111
₩22/1A B73/7-4	HVDID 11111 HVDID 11111	PAEIG 11111 PAEIG 11111	KNKQP 11111 KNKQP	HVSIC 11111 HVSIC 11111	ADVKL 11111 ADVKL	ALQGM 11111 ALQGM 11111	NALLE 11111 NALLE 11111	GS12K 11111 GS12K GS12K	KSFDF 11111 KSFDF 11111	11111 62AND 11111 62AND	ELDQQ 11111 ELDQQ 11111	KREFP 11111 KREFP 11111 KREFP
₩22/1A B73/7-4	HVDID 11111 HVDID 11111 HVDID	PAEIG PAEIG 11111 PAEIG 11111 PAEIG 430	KNKQP 11111 KNKQP 11111 KNKQP	HVSIC 11111 1421C 11111 1421C 11111 1421C	ADYKL 11111 ADYKL 11111 ADYKL	ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450	NALLE 11111 NALLE 11111 NALLE	GSTSK 11111 GSTSK 11111 GSTSK	KSFDF 11111 KSFDF 11111 KSFDF	GSYND GSYND 11111 GSYND 11111 GSYND	ELDQQ 11111 ELDQQ 11111 ELDQQ	KREFP 11111 KREFP 11111 KREFP 480
H22/1A B73/7-4 XI12/8A	FRANCE FR	PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI	KNKQP 11111 KNKQP 11111 KNKQP QPQYA	HAZIC 11111 HAZIC 11111 HAZIC 11111 HAZIC 10AFD	ADYKL 11111 ADYKL 11111 ADYKL ELTKG	ALOGH ALOGM 11111 ALOGM 11111 ALOGM 450 EATIG	NALLE 11111 NALLE 11111 NALLE TGVGQ	GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA	KSFDF 11111 KSFDF 11111 KSFDF AQYYT	GSYND GSYND 11111 GSYND 11111 GSYND 470 YKRPR	OAF22 OAF22 11111 EFD00 11111 EFD00	KREFP 11111 KREFP 11111 KREFP 480 AGLGA
H22/1A B73/7-4 XI12/8A XI12/8A	FRANCE TO THE PROPERTY OF THE	PAEIG 11111 PAEIG 11111 PAEIG 430 SNEEI SNEEI 11111 SNEEI	KNKQP 11111 KNKQP 11111 KNKQP QPQYA QPQYA 11111 QPQYA	HAZIC 11111 HAZIC 11111 HAZIC 10AГD 11111 11111 10AГD	ADYKL 11111 ADYKL 11111 ADYKL ELTKG 11111 ELTKG	ALOGH ALOGM 11111 ALOGM 450 EATIG 11111 EATIG	NALLE 11111 NALLE 11111 NALLE TGVGQ 11111 TGVGQ	GSTSK GSTSK 11111 GSTSK 11111 GSTSK 460 HQMYA	KSFDF 11111 KSFDF 11111 KSFDF AQYYT AQYYT 11111 AQYYT	GSYND GSYND 11111 GSYND 11111 GSYND 470 YKRPR YKRPR 11111 YKRPR	OAF22 0AF22 11111 EFD00 111111 EFD00	KREFP 11111 KREFP 11111 KREFP 480 AGLGA AGLGA 11111 AGLGA

	490	500	510	520	530	540
X112/8A	MGFGL PAAAG	ASVAN PGVTV	YDIDG DGSFL	MNVQE LAMIR	IENLP VKVFV	LNNOH LGHVV
#22/1A	MGFGL PAAAG	ASVAN PGVTV	VDIDG DGSFL	MNVQE LAMIR	IENLP VKVFV	LNNQH LGMVV
	11111 11111	11111 11111	111111 111111	11111 11111	11111 11111	11111 11111
B73/7-4	MGFGL PAAAG	ASVAN PGVTV	VDIDG DGSFL	MNVQE LAMIR	IENLP VKVFV	<b>LUNGH LGMAA</b>
		11111 11111				
XI12/8A	MGFGL PAAAG	ASVAN PGVTV	VDIDG DGSFL	MNVQE LAMIR	IENLP VKVFV	LNNOH LGMVV
	FFA	E/ A	F70	Γ00	504	
	550			580		
XI12/8A	QHEDR FYKAN	RAHTY LGNPE	NEZEI Abdea	TIAKG FNIPA	AKAIK KWEAK	AAIKK MLETP
₩22/1A	UNLUD LANVI	RAHTY LGNPE	אבנבו אסטבה	TIAVE ENIDA	VDVTV VNEVD	AAIVY MICTO
מככו וא		11111 11111				
D70/7 4						11111 11111
B73/7-4		RAHTY LGNPE				
		11111 11111				
XI12/8A	QYEDR FYKAN	RAHTY LGNPE	NESEI YPDFV	TIAKG FNIPA	AKALK KNEAK	AAIKK MLETP
	610	620	630			
VI 12 /04				nenen tuv		
XI12/8A	CLIFF DILAL	HQEHV LPMIP	NUUAT RUMIL	אטעטע אויא		
422/1A	GPYLL DIIVP	HOEHV LPMIP	sGGAF KDMIL	DGDGR TVY>		
	11111 11111	11111 11111	11111 11111	11111 111		
B73/7-4	GPYLL DIIVP	HQEHV LPMIP	sGGAF KDMIL	DGDGR TVY>		
·	11111 11111	11111 11111	1111 11111	11111 111		
X112/8A		HQEHV LPMIP				
	G ILL DIII		MAGIN NUMBE	ווי אוטעטע		

FIG.8C